

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: February 1, 2002, 09:56:24 ; Search time 24.48 Seconds

(without alignments)  
502.831 Million cell updates/sec

Title: US-09-378-759-11\_COPY\_1\_547

Sequence: 1 LLAVEETLMDSTATAELG.....IIGSSAGVFLIAVYVIAI 547

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCRTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2895	100.0	970 2	US-08-449-645A-11 Sequence 11, Appl
2	2895	100.0	970 2	US-08-702-367A-11 Sequence 11, Appl
3	2895	100.0	970 5	PCT-US95-04681-11 Sequence 11, Appl
4	2870	99.1	994 4	US-08-542-635-2 Sequence 2, Appl
5	2785	96.2	995 1	US-08-162-809-18 Sequence 18, Appl
6	2785	96.2	1011 1	US-08-162-809-12 Sequence 12, Appl
7	2758	95.3	995 2	US-08-673-789-5 Sequence 5, Appl
8	2087.5	72.1	984 2	US-08-673-789-6 Sequence 6, Appl
9	1898.5	65.6	951 1	US-08-162-809-2 Sequence 2, Appl
10	1804	62.3	973 1	US-08-162-809-14 Sequence 14, Appl
11	1804	62.3	988 1	US-08-162-809-14 Sequence 14, Appl
12	1800.5	62.2	998 2	US-08-449-645A-20 Sequence 20, Appl
13	1800.5	62.2	998 2	US-08-449-645A-20 Sequence 20, Appl
14	1800.5	62.2	998 5	PCT-US95-04681-20 Sequence 20, Appl
15	1765.5	61.0	993 1	US-08-348-143-1 Sequence 8, Appl
16	1765.5	61.0	993 1	US-08-571-785-1 Sequence 1, Appl
17	1765.5	61.0	993 4	US-09-192-435-1 Sequence 1, Appl
18	1761.5	60.8	970 2	US-08-673-789-7 Sequence 7, Appl
19	1675.5	57.9	973 2	US-08-162-809-8 Sequence 8, Appl
20	1485.5	51.3	967 2	US-08-449-645A-30 Sequence 30, Appl
21	1485.5	51.3	967 2	US-08-702-367A-10 Sequence 30, Appl
22	1485.5	51.3	991 2	US-08-449-645A-13 Sequence 13, Appl
23	1485.5	51.3	991 2	US-08-702-367A-13 Sequence 13, Appl
24	1485.5	51.3	991 5	PCT-US95-04681-13 Sequence 13, Appl
25	1481	51.2	1005 2	US-08-469-537A-103 Sequence 103, Appl
26	1476.5	51.0	983 2	US-08-167-919A-10 Sequence 10, Appl
27	1476.5	51.0	983 2	US-08-449-645A-21 Sequence 21, Appl

28	1476.5	51.0	983 2	US-08-702-367A-21 Sequence 21, Appl
29	1476.5	51.0	983 3	US-08-715-106-10 Sequence 10, Appl
30	1476.5	51.0	983 5	PCT-US95-04681-21 Sequence 21, Appl
31	1474.5	50.9	983 1	US-08-162-809-16 Sequence 16, Appl
32	1472.5	50.9	986 2	US-08-673-789-3 Sequence 3, Appl
33	1468.5	50.7	986 2	US-08-449-645A-15 Sequence 15, Appl
34	1468.5	50.7	986 2	US-08-702-367A-15 Sequence 15, Appl
35	1468.5	50.7	986 5	PCT-US95-04681-15 Sequence 15, Appl
36	1466	50.6	982 2	US-08-673-789-4 Sequence 4, Appl
37	1461.5	50.5	1104 1	US-08-222-616-36 Sequence 36, Appl
38	1461.5	50.5	1104 5	PCT-US95-04228-36 Sequence 36, Appl
39	1455	50.3	998 2	US-08-449-645A-17 Sequence 17, Appl
40	1455	50.3	998 2	US-08-702-367A-17 Sequence 17, Appl
41	1455	50.3	998 5	PCT-US95-04681-17 Sequence 17, Appl
42	1453.5	50.2	993 4	US-08-368-776A-11 Sequence 11, Appl
43	1446	49.9	610 4	US-08-368-776A-3 Sequence 3, Appl
44	1446	49.9	610 5	PCT-US96-00419-3 Sequence 3, Appl
45	1446	49.9	626 4	US-08-368-776A-5 Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-08-449-645A-11  
; Sequence 11, Application US/08449645A  
; Patent No. 5981245  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/449,645A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 970 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-449-645A-11

Query Match 100.0%; Score 2895; DB 2; Length 970;  
Best Local Similarity 100.0%; Pred. No. 5.5e-246;  
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAVEETLMDSTATAELGVMVHPGSGMEVSGDENMNTIRFYOVCMVFESSQNNMLR 60  
DB 1 LLAVEETLMDSTATAELGVMVHPGSGMEVSGDENMNTIRFYOVCMVFESSQNNMLR 60  
QY 61 TKFTRRGARRIHVEMKFSYRDGSSIPVSGCKETFNLYYEADPDSATKTPNNMNP 120  
DB 61 TKFTRRGARRIHVEMKFSYRDGSSIPVSGCKETFNLYYEADPDSATKTPNNMNP 120  
QY 121 WVKVDITADESFQVDLGGKRVKINTEVRSFGPVNSGRTYLAFOYGGCMSLIAVRFY 180

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Db 121 WVKVDTIADESFQVDLAGRVKMTIEVRSFGVSRSGFTLAFODYGGCMLIAVRFY 180  
OY 181 RKCPRIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPILKXCGDGMVLPIGR 240  
Db 181 RKCPRIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPILKXCGDGMVLPIGR 240  
OY 241 MCKAGFEAVENGTCVRCGCPSTFRKANOGEACHTCPINSRTSSEATNCVCRNGYTRADL 300  
Db 241 MCKAGFEAVENGTCVRCGCPSTFRKANOGEACHTCPINSRTSSEATNCVCRNGYTRADL 300  
OY 301 DPLDMCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGRGACTR 360  
Db 301 DPLDMCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGRGACTR 360  
OY 361 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTITNOA 420  
Db 361 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTITNOA 420  
OY 421 APSAVSIMHOVSTVDSITLSWSQDPONGVILIDYELQYKEKELSEYNATAIKSPNTVT 480  
Db 421 APSAVSIMHOVSTVDSITLSWSQDPONGVILIDYELQYKEKELSEYNATAIKSPNTVT 480  
OY 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEYQTSIOEKPLIIGSSAAGLVFLI 540  
Db 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEYQTSIOEKPLIIGSSAAGLVFLI 540  
OY 541 AVVVIAT 547  
Db 541 AVVVIAT 547  
RESULT 2  
US-08-702-367A-11  
Sequence 11, Application US/08702367A  
Patent No. 5981246  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702.367A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 970 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-702-367A-11  
Query Match 100.0%; Score 2895; DB 2; Length 970;  
Best Local Similarity 100.0%; Pred. No. 5.5e-246;  
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LLAAVEETIMDSSTATAELGMMVHPSPGMEVEYSGYDENNTIRTYQVCNVSESSQNNMLR 60  
Db 1 LLAAVEETIMDSSTATAELGMMVHPSPGMEVEYSGYDENNTIRTYQVCNVSESSQNNMLR 60  
OY 61 TKFTRRGARHRIHVEKFSYRDCSSIPSVGSCKETFNLYYYEADPDSATKTFPMWENP 120  
Db 61 TKFTRRGARHRIHVEKFSYRDCSSIPSVGSCKETFNLYYYEADPDSATKTFPMWENP 120  
OY 121 WVKVDTIADESFQVDLAGRVKMTIEVRSFGVSRSGFTLAFODYGGCMLIAVRFY 180  
Db 121 WVKVDTIADESFQVDLAGRVKMTIEVRSFGVSRSGFTLAFODYGGCMLIAVRFY 180  
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Db 181 RKCPRIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPILKXCGDGMVLPIGR 240  
OY 241 MCKAGFEAVENGTCVRCGCPSTFRKANOGEACHTCPINSRTSSEATNCVCRNGYTRADL 300  
Db 241 MCKAGFEAVENGTCVRCGCPSTFRKANOGEACHTCPINSRTSSEATNCVCRNGYTRADL 300  
OY 301 DPLDMCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGRGACTR 360  
Db 301 DPLDMCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGRGACTR 360  
OY 361 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTITNOA 420  
Db 361 CGDNVQYAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPSPQFASVNTITNOA 420  
OY 421 APSAVSIMHOVSTVDSITLSWSQDPONGVILIDYELQYKEKELSEYNATAIKSPNTVT 480  
Db 421 APSAVSIMHOVSTVDSITLSWSQDPONGVILIDYELQYKEKELSEYNATAIKSPNTVT 480  
OY 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEYQTSIOEKPLIIGSSAAGLVFLI 540  
Db 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEYQTSIOEKPLIIGSSAAGLVFLI 540  
OY 541 AVVVIAT 547  
Db 541 AVVVIAT 547  
RESULT 3  
PCT-US95-04681-11  
Sequence 11, Application PC/TUS9504681  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04681  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 970 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein  
PCT-US95-04681-11

Query Match 100.0% Score 2895; DB 5; Length 970;  
Best Local Similarity 100.0%; Pred. No. 5.5e-246;  
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAVEETLMDSTTAATAGLGMVHPPSGMEVSGYDENMTIRTYOVAVFESSQNNMLR 60  
DB 1 LLAVEETLMDSTTAATAGLGMVHPPSGMEVSGYDENMTIRTYOVAVFESSQNNMLR 60  
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DB 61 TKTIRRGARHRIHVEKESVRCSSIPVSGCKETFNLYYEADDSATKTFPMNMENP 120  
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DB 121 WVKVDTIADESEFQVLDGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 180  
QY 181 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPKILYCNDEGEMLVPIGR 240  
DB 181 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPKILYCNDEGEMLVPIGR 240  
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DB 241 MCKAGEAVENGTVCRCGSGTFKANOGEACTHCPINSRTTSECATNCVCNNGYRADL 300  
QY 301 DPLDMCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGSGGACTR 360  
DB 301 DPLDMCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGSGGACTR 360  
QY 361 CGDNVOYAPROGLTEPRITISDLAHTQYFEIOAVNGVTDQSPFSPQFASVNTTNOA 420  
DB 361 CGDNVOYAPROGLTEPRITISDLAHTQYFEIOAVNGVTDQSPFSPQFASVNTTNOA 420  
QY 421 APSAVSIMHOVSRTVDSITLSMSOPDQNGVILDELYEKEKSEYNATIKSPNTVT 480  
DB 421 APSAVSIMHOVSRTVDSITLSMSOPDQNGVILDELYEKEKSEYNATIKSPNTVT 480  
QY 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEAYQTSIOEKLPLIIGSSAAGLVFLI 540  
DB 481 GLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEAYQTSIOEKLPLIIGSSAAGLVFLI 540  
QY 541 AVVIVAI 547  
DB 541 AVVIVAI 547

US-08-542-635-2  
Sequence 2, April 1998, US/08542635  
Patent No. 6,238,956  
GENERAL INFORMATION:  
APPLICANT: PAVSON, Anthony  
APPLICANT: Henkemeier, Mark  
APPLICANT: Letwin, Kenneth  
TITLE OF INVENTION: NOVEL NEURAL RECEPTOR  
TITLE OF INVENTION: TYROSINE KINASE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: Bereskin & Parr  
STREET: 40 King Street West, Box 401  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 3Y2

CLMm 2  
seq ID 2  
26-548  
4/29/94  
CLMm 5  
priority  
76

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/542,635  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: McDiarmid, Shona S.  
REGISTRATION NUMBER: 38,798  
REFERENCE/DOCKET NUMBER: 3153-162  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 364-7311  
TELEFAX: (416) 361-1398  
TELEX: 06-23115  
INFORMATION FOR SRO ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 994 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
DEVELOPMENTAL STAGE: Embryo  
IMMEDIATE SOURCE:  
LIBRARY: lambda gt10 cDNA library  
CLONE: Combined pNURACE A2 and K2 and cDNA clones  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: Distal end of chromosome 4  
MAP POSITION: near the and-1 mutation  
US-08-542-635-2

Query Match 99.1% Score 2870; DB 4; Length 994;  
Best Local Similarity 98.9%; Pred. No. 8.9e-244;  
Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 1 LLAVEETLMDSTTAATAGLGMVHPPSGMEVSGYDENMTIRTYOVAVFESSQNNMLR 60  
DB 23 LLAVEETLMDSTTAATAGLGMVHPPSGMEVSGYDENMTIRTYOVAVFESSQNNMLR 82  
QY 61 TKTIRRGARHRIHVEKESVRCSSIPVSGCKETFNLYYEADDSATKTFPMNMENP 120  
DB 83 TKTIRRGARHRIHVEKESVRCSSIPVSGCKETFNLYYEADDSATKTFPMNMENP 142  
QY 121 WVKVDTIADESEFQVLDGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 180  
DB 143 WVKVDTIADESEFQVLDGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 202  
QY 181 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPKILYCNDEGEMLVPIGR 240  
DB 203 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPKILYCNDEGEMLVPIGR 262  
QY 241 MCKAGEAVENGTVCRCGSGTFKANOGEACTHCPINSRTTSECATNCVCNNGYRADL 300  
DB 263 MCKAGEAVENGTVCRCGSGTFKANOGEACTHCPINSRTTSECATNCVCNNGYRADL 322  
QY 301 DPLDMCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGSGGACTR 360  
DB 323 DPLDMCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGSGGACTR 382  
QY 361 CGDNVOYAPROGLTEPRITISDLAHTQYFEIOAVNGVTDQSPFSPQFASVNTTNOA 420  
DB 383 CGDNVOYAPROGLTEPRITISDLAHTQYFEIOAVNGVTDQSPFSPQFASVNTTNOA 442  
QY 421 APSAVSIMHOVSRTVDSITLSMSOPDQNGVILDELYEKEKSEYNATIKSPNTVT 480  
DB 443 APSAVSIMHOVSRTVDSITLSMSOPDQNGVILDELYEKEKSEYNATIKSPNTVT 502  
QY 481 --GLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEAYQTSIOEKLPLIIGSSAAGLVFLI 538  
DB 503 VGLKAGAIYFQVARTVAGYGRYSGKMYFQMTAEAYQTSIOEKLPLIIGSSAAGLVFLI 562  
QY 539 LIAVVIVAI 547  
DB 563 LIAVVIVAI 571

RESULT 5  
US-08-162-809-18  
Sequence 18, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
NUMBER OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 995 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-162-809-18

Query Match 96.2%; Score 2785; DB 1; Length 995;  
Best Local Similarity 94.5%; Pred. No. 2.7e-236;  
Matches 519; Conservative 19; Mismatches 9; Indels 2; Gaps 1;

QY 1 LLAVEETLMDSTTATATLGMVHPSPSGWEVSGYDENMNTIRTYOVCAVFESSQNNMLR 60  
DB 23 LLAVEETLMDSTTATATLGMVHPSPSGWEVSGYDENMNTIRTYOVCAVFESSQNNMLR 82  
QY 61 TKFIRRGARIRIHEMKFSVRDCSSIPVPGSCKETFNLYYEADPDSATKTFPNMNEP 120  
DB 83 TKYIRRGARIRIHEMKFSVRDCSSIPVPGSCKETFNLYYEADPDSATKTFPNMNEP 142  
QY 121 WVKVDITLADSEFSQVULGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMSLIAVRVY 180  
DB 143 WVKVDITLADSEFSQVULGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMSLIAVRVY 202  
QY 181 RKCPRIIONGAIFQETLSGASTSLVAARGSCIANAEVDVPIKLYONGDEMLVPIGRG 240  
DB 203 RKCPRIIONGAIFQETLSGASTSLVAARGSCIANAEVDVPIKLYONGDEMLVPIGRG 262  
QY 241 MCKAGFEVNGTVCRCGPSTGFRANOGDEACTHCPINRSTSGAATNCVCNRYRADL 300  
DB 263 MCKAGFEVNGTVCRCGPSTGFRANOGDEACTHCPINRSTSGAATNCVCNRYRADL 322  
QY 301 DPLDPCCTTISAPQAVISSVNETSIMLEMTPPRDSGGRDLVYNIICKSGSGGACTR 360  
DB 323 DPLDPCCTTISAPQAVISSVNETSIMLEMTPPRDSGGRDLVYNIICKSGSGGACTR 382  
QY 361 CGDNVQVAPROLGLTEPRITISDLIAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 420

Dec. 3, 1993

DB 383 CGDNVQVAPROLGLTEPRITISDLIAHTQYTFEIOAVNGVTDQSPFSPQFASVNTTNOA 442  
QY 421 APSAVSIMHOVSRVDSITLWSOPDOPNGVILDIYQYKEKLESENAIRASPTNTV 480  
DB 443 APSAVSIMHOVSRVDSITLWSOPDOPNGVILDIYQYKEKLESENAIRASPTNTV 502  
QY 481 --GKAGATVYQVARTVAGYGRYSKMYEQMTTEAEOSTIOEKPLIIGSSAGLVF 538  
DB 503 VQNKAGTIVYQVARTVAGYGRYSKMYEQMTTEAEOSTIOEKPLIIGSSAGLVF 562  
QY 539 LIAVVIAT 547  
DB 553 LIAVVIAT 571

RESULT 6  
US-08-162-809-12  
Sequence 12, Application US/08162809  
Patent No. 5457048  
GENERAL INFORMATION:  
APPLICANT: Pasquale, Elena B.  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
NUMBER OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,809  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LJ 9503  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1011 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-162-809-12

Query Match 96.2%; Score 2785; DB 1; Length 1011;  
Best Local Similarity 94.5%; Pred. No. 2.7e-236;  
Matches 519; Conservative 19; Mismatches 9; Indels 2; Gaps 1;

QY 1 LLAVEETLMDSTTATATLGMVHPSPSGWEVSGYDENMNTIRTYOVCAVFESSQNNMLR 60  
DB 23 LLAVEETLMDSTTATATLGMVHPSPSGWEVSGYDENMNTIRTYOVCAVFESSQNNMLR 82  
QY 61 TKFIRRGARIRIHEMKFSVRDCSSIPVPGSCKETFNLYYEADPDSATKTFPNMNEP 120  
DB 83 TKYIRRGARIRIHEMKFSVRDCSSIPVPGSCKETFNLYYEADPDSATKTFPNMNEP 142  
QY 121 WVKVDITLADSEFSQVULGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMSLIAVRVY 180  
DB 143 WVKVDITLADSEFSQVULGGRVAKINTEVRSFGPVSRSGFYLAFOYGGCMSLIAVRVY 202

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OY 181 RCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGBNLPICRC 240
DB 203 RCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGBNLPICRC 262
OY 241 MCKAGEAVENGTCVRCGCPGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 300
DB 263 MCKAGEAVENGTCVRCGCPGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 322
OY 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGGACATR 360
DB 323 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGGACATR 382
OY 361 CGDNVOYAPROLGTEPRITISDLAHTQYTFEIOAVNGVTDOSFSPQFASVNTTNOA 420
DB 383 CGDNVOYAPROLGTEPRITISDLAHTQYTFEIOAVNGVTDOSFSPQFASVNTTNOA 442
OY 421 APSAIVSIMHOVSRTVDSITLSMSOPDQNGVILDELOYEKEKELSEYNATAIKSPNTVT 480
DB 443 APSAIVSIMHOVSRTVDSITLSMSOPDQNGVILDELOYEKEKELSEYNATAIKSPNTVT 502
OY 481 --GLKAGAIYFOVARARTVAGYGRYSKMYFOTMTEAEYOTSIQEKPLIIGSSAAGLVF 538
DB 503 VONLAKAGTIYFOVARARTVAGYGRYSKMYFOTMTEAEYOTSIQEKPLIIGSSAAGLVF 562
OY 539 LIAVVYIAI 547
DB 563 LIAVVYIAI 571

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524, 1994

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RESULT 7
US-08-673-789-5
; Sequence 5, Application US/08673789
; Patent No. 5814479
; GENERAL INFORMATION:
; APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
; APPLICANT: GEORGE, F.
; TITLE OF INVENTION: BSK RECEPTOR LIKE
; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/673,789
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/177,812
; FILING DATE: 04-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4105
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO. 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 995

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; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; US-08-673-789-5

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Query Match 95.3%; Score 2758; DB 2; Length 995;
Best Local Similarity 93.6%; Pred. No. 6,3e-234;
Matches 514; Conservative 19; Mismatches 14; Indels 2; Gaps 1;

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OY 1 LIAVEETLNDSTTATPELGMVHPSPGMEVSGYDENMTITTYOVCNFPESONNMLR 60
DB 23 LIAVEETLNDSTTATPELGMVHPSPGMEVSGYDENMTITTYOVCNFPESONNMLR 82
OY 61 TKFIRRRGAHRIHEMKFSVRDCSSIPSVSGCKETFNLYEADPDATKTPNNMNP 120
DB 83 TKYIRRRGAHRIHEMKFSVRDCSSIPNVGSKCKEFLNLYESDDSDATKTPNNMNP 142
OY 121 WNVVDITAADESFQVDLGRVVKINTEVRSFGPVSRSGFYLAFOYGCMSLIAVRY 180
DB 143 WNVVDITAADESFQVDLGRVVKINTEVRSFGPVSRSGFYLAFOYGCMSLIAVRY 202
OY 181 RCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGBNLPICRC 240
DB 203 RCPRIIONGAIFQETLSGAESTSLVAARGSCIANAEVDVPKLYCNGDGBNLPICRC 262
OY 241 MCKAGEAVENGTCVRCGCPGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 300
DB 263 MCKAGEAVENGTCVRCGCPGSGTFKANOGEACTHCPINSRTTSEGATNCVCRNGYRADL 322
OY 301 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGGACATR 360
DB 323 DPLDMPCTTIPSAPOAVISSVNETSLMEWTPPRDSGREDLVYNIICKSCSGGACATR 382
OY 361 CGDNVOYAPROLGTEPRITISDLAHTQYTFEIOAVNGVTDOSFSPQFASVNTTNOA 420
DB 383 CGDNVOYAPROLGTEPRITISDLAHTQYTFEIOAVNGVTDOSFSPQFASVNTTNOA 442
OY 421 APSAIVSIMHOVSRTVDSITLSMSOPDQNGVILDELOYEKEKELSEYNATAIKSPNTVT 480
DB 443 APSAIVSIMHOVSRTVDSITLSMSOPDQNGVILDELOYEKEKELSEYNATAIKSPNTVT 502
OY 481 --GLKAGAIYFOVARARTVAGYGRYSKMYFOTMTEAEYOTSIQEKPLIIGSSAAGLVF 538
DB 503 VONLAKAGTIYFOVARARTVAGYGRYSKMYFOTMTEAEYOTSIQEKPLIIGSSAAGLVF 562
OY 539 LIAVVYIAI 547
DB 563 LIAVVYIAI 571

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RESULT 8
US-08-673-789-6
; Sequence 6, Application US/08673789
; Patent No. 5814479
; GENERAL INFORMATION:
; APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
; APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
; APPLICANT: GEORGE, F.
; TITLE OF INVENTION: BSK RECEPTOR LIKE
; TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
; TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK

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QY 76 MKFSYRDCSSLPSPGCKEFTFNLYTADDFOSATITPPNMENMFWVDTIADDEFSQ 135
Db 81 LKFTYDDNCSSIPNIPGCKEFTFNLEYESDTOSASANSFPMENNY IYVDIADDEFSK 140
QY 136 VDLGGVWKMINEVFSFGPSRSGEFTYLAFDYDGGCSLLAVVFRKCPRIIIONGAIFQ 195
Db 141 LBSG-----RVNFKVHSFEPILSKNFTYLAFDQDAGCSLLISVAFKCKSNTIAGAFIPE 196
QY 196 TUSGASTSLVAAGSCIANAEVDVFIKLYCNGDGBMLYPIGRMCCKAGFEAVENGVC 255
Db 197 TLTGAPETSLVLAPOCTCPNAAEVSVPLKLYCNGDEBMMVPAGACTCAAGIPEAMKDTQC 256
QY 256 RGGPSTFEFANGDGAETHCPIINRITSEBAGTNCVCGNCRYRADDLPLDMPCTITPSAPQ 315
Db 257 QACGPEFTFSKSGEBCPCPCPNRSRTTAAATYV ICGSGFEFRADPADPADSACTSVSADR 316
QY 316 AVTSSVNETSLMLEMTPPRDSGREDLYNITICKSCSGSGAGACTRCGDMMVOYVAPQL--- 372
Db 317 SVTSSNNEFTSLVLEWSEPDAGGRDILLYNTICKCSVERELICSDDDVVEVPQOLGT 373
QY 373 GLEPEPRTYISDLAHTQYTFEIOANGVTDSPSPSFASVNTITTOAPASAVSIMHOVS 433
Db 377 GLTERRTIYSKWAHHQYTFEIOANGTSSSPYPRHFAVNTITTOAPASAVPTMHHS 434
QY 433 RYVDSITLWSOPDOPNGVILDELYQYERE-LEBYNAATIKSEPTYV---TGKKGALYV 488
Db 437 STGSKMSTLWTPPERNGIILDIETKYESEKGGGDGLANTVTSQKNSVRDLGKAKARMT 491
QY 490 FOVARAVAGYSGSKMFEOMTFAEQTISOERLLITIGSSAAGIVELLAVVTAI 547
Db 497 VQVAKRYVAGYGRSLPTEFQTTADGSGSTKTPQELPLIYGSATAGLLFVIVVTAI 554

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Query Match	62.28;	Score 1800.5;	DB 2;	Length 998;
Best Local Similarity	61.98;	Pred. No. 1e-149;		

Matches	340;	Conservative	79;	Mismatches	119;	Indels	11;	Gaps	5
QY	4	AVEETLMDSTATAELGMVHPHPSGMEVSYSDENMTIRTYQVCNFFSSONNNWLR	63						
Db	37	ALAEETLMDTKWVTSLEATWTSHPESGMEVSYSDENMPIRFYQVCNRESSONNNWLTGCF	96						
QY	64	IRRGCAHRIHVMEKRSYVDCSSIPVPSCKEETENLYXEADFPDAIKTPPMNMEHPWK	123						
Db	97	IMRDVQRYVELKTFETDCCNSIPNPBSCKETRIPLFYEADSDVYASASSPFMMENYDK	156						
QY	124	VDTIADSEFSQVDLGGHYMKINTERVSEFVSRSGFYLAFODYGGCKSLIAAVRYTRKC	183						
Db	157	VDTIADSEFSRLDAG---RVNTRKVRSEFPLSKAGFYLAFODQACMSLIVAFYKRC	212						
QY	184	PRITONGAIFQETLSAISTSVYARGSGIENAEVDVPIKLYCNGDEMLVPIGRCMCK	243						
Db	213	ASTTAGFAFPELTIGALTESLVIAPGTCIPNAVYVSYPLIKYCNGDEMMVPIGACATCA	272						
QY	244	AGFEAVENGTVCRCGCPSGYFKKANOCDDEACTHCPINSRFTSBCATNCVCRCNGTYADIDL	303						
Db	273	TGHEPRAPKESQCPGCPSPSYKAKOGGRLCPPLCPMNSRTSPAAISICTCHNNFTRADSDSA	332						
QY	304	DMECTTIPSPAPAVISVNETSLMLEMTPRPBGSGREPLVNIITCKSC--GSGGACATRC	361						
Db	333	DSACTVYSPSPRCVIVSNVETSLILEMSPRGLGVARDLLIYVICKKHGGAGGASACRC	392						
QY	362	GDAVQVAPRLGLTEPRITSLDLATQYTFELQVANGVTDSPSPQFASVNIITNOAA	421						
Db	393	DDNVEFPRDLGISEPRVHSHLLATRTTFEVOANGVSGKSPLPBPRAVNIITNOAA	452						
QY	422	PSAAYSIMHOVSRVDSITLSWSQPDQPNVYILDYELQYIEKELSEYNATKISPTNIV--	479						
Db	453	PSEVPTRLRHSSGSSSITSLMAPPEPNVYIIDYEMKRYEK--SGSIASTYSQNNSQL	510						
QY	480	TGLKAGLIYFQVQARARVAVAGRYGSKMYEFOQWTE-AEYQTSIOEKLPLITGSSAAGLV	538						
Db	511	DGLRDPARVYQVAVARVAGYGOYSRPAEFETTSSENGSAQOQLQRLPLIVGSAATAGLV	570						
QY	539	LIAYVVAI 547							
Db	571	VYAVVVAI 579							

RESULT 13  
 ; Sequence 20, Application US/08702367A  
 ; US-08-702-367A-20  
 ; Patent No. 5981246  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fox, Gary M.  
 ; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
 ; TITLE OF INVENTION: Kinases  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Amgen Patent Operations/RBW  
 ; STREET: 1840 Dehavilland Drive  
 ; CITY: Thousand Oaks  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 91320  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/702,367A  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Winter, Robert B.  
 ; REFERENCE/DOCKET NUMBER: A-287  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:



LENGTH: 998 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-702-367A-20

Query Match 62.2%; Score 1800.5; DB 2; Length 998;  
Best Local Similarity 61.9%; Pred. No. 1e-149;  
Matches 340; Conservative 79; Mismatches 119; Indels 11; Gaps 5;

QY 4 AVEETLMDSTTATAEIGMWHPPSGMEVSGYDENNTIRTYOVCNVPRESSONNMRLRTKF 63  
DB 37 ALEETLMDTKWTSLELAWTSHPSGMEVSGYDEAMNPIRTYOVNVPRESSONNMRLRTGF 96  
QY 64 IRRGAHRIHVEKESVNDCCSIPVSGCKETFNLYYEADFDSTAKTFPMNMENPMVK 123  
DB 97 IWRDQVQRYVELKFTYVDCNSIPNIPSGCKETFNLYYEADSDVASASPMMENPMYK 156  
QY 124 VDTIADESFQVDLGGVWKINTEVSRGPGVSRSGFYLAPODYGCMGLAVAFYRKC 183  
DB 157 VDTIAPDSFRLDAG---RVNTKVRSGFPLSKAGFYLAPODQACMSLISVRAFYRKC 212  
QY 184 PRIIONGAIFOETLSGAEVSTLVAARGSCIANAEVDVPIKLYCNGDEMLVPIGRCK 243  
DB 213 ASTYAGFALFPETLGAEPSTLVIAPGTCIPNAVEVSVPKLYCNGDEMLVPIGACTCA 272  
QY 244 AGFEAVENGTVRCGPGSTFRKANGDEACTHCPINSTTSEGATNCYCRNGYTRADLPL 303  
DB 273 TGHPRAKSQCRCPCPGSTFRKANGDEACTHCPINSTTSEGATNCYCRNGYTRADLPL 303  
QY 304 DMCPTTIPSAPOAVISSVNETSLALEMTPPRDSGREDLVYNIICKSC--GSGRAGACTRC 361  
DB 333 DSACTTVPSPRGVYSVNETSLILEMSEPRDLGVRDLLVNIICKCHGAGASACSRK 392  
QY 362 GDNVQYAPROLGLTPRIYISDLAHQYTFEIQAVNGVTDOSPSPQASVNTTNOAA 421  
DB 393 DNVVEFVPRQLGLSEPRVHTSHLAHTRYFEVQAVNGVSGKSPPLRYAAVNTTNOAA 452  
QY 422 PSAVSIHQVSRVDSITLMSOPDOPNGVILDELOYKEKLSYNAITAKSPNTV-- 479  
DB 453 PSEVPTLRLHSSGSSSLTSLNAPPERNGVILDEYEMKFEK--SEGIASTYTSOMNSVOL 510  
QY 480 TGLKAGAIYFQVRAVYAGYRGSKMYFQMTAEYQTSIOEKPLITIGSSAAGLV 538  
DB 511 DGLRPARYVQVRAVYAGYRGSKMYFQMTAEYQTSIOEKPLITIGSSAAGLV 570  
QY 539 LIAVVYVIAI 547  
DB 571 VVAVVYVIAI 579

RESULT 14  
PCT-US95-04681-20  
Sequence 20, Application PC/TUS9504681  
GENERAL INFORMATION:

APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavenland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04681  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 998 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-04681-20

Query Match 62.2%; Score 1800.5; DB 5; Length 998;  
Best Local Similarity 61.9%; Pred. No. 1e-149;  
Matches 340; Conservative 79; Mismatches 119; Indels 11; Gaps 5;

QY 4 AVEETLMDSTTATAEIGMWHPPSGMEVSGYDENNTIRTYOVCNVPRESSONNMRLRTKF 63  
DB 37 ALEETLMDTKWTSLELAWTSHPSGMEVSGYDEAMNPIRTYOVNVPRESSONNMRLRTGF 96  
QY 64 IRRGAHRIHVEKESVNDCCSIPVSGCKETFNLYYEADFDSTAKTFPMNMENPMVK 123  
DB 97 IWRDQVQRYVELKFTYVDCNSIPNIPSGCKETFNLYYEADSDVASASPMMENPMYK 156  
QY 124 VDTIADESFQVDLGGVWKINTEVSRGPGVSRSGFYLAPODYGCMGLAVAFYRKC 183  
DB 157 VDTIAPDSFRLDAG---RVNTKVRSGFPLSKAGFYLAPODQACMSLISVRAFYRKC 212  
QY 184 PRIIONGAIFOETLSGAEVSTLVAARGSCIANAEVDVPIKLYCNGDEMLVPIGRCK 243  
DB 213 ASTYAGFALFPETLGAEPSTLVIAPGTCIPNAVEVSVPKLYCNGDEMLVPIGACTCA 272  
QY 244 AGFEAVENGTVRCGPGSTFRKANGDEACTHCPINSTTSEGATNCYCRNGYTRADLPL 303  
DB 273 TGHPRAKSQCRCPCPGSTFRKANGDEACTHCPINSTTSEGATNCYCRNGYTRADLPL 303  
QY 304 DMCPTTIPSAPOAVISSVNETSLALEMTPPRDSGREDLVYNIICKSC--GSGRAGACTRC 361  
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DB 393 DNVVEFVPRQLGLSEPRVHTSHLAHTRYFEVQAVNGVSGKSPPLRYAAVNTTNOAA 452  
QY 422 PSAVSIHQVSRVDSITLMSOPDOPNGVILDELOYKEKLSYNAITAKSPNTV-- 479  
DB 453 PSEVPTLRLHSSGSSSLTSLNAPPERNGVILDEYEMKFEK--SEGIASTYTSOMNSVOL 510  
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DB 571 VVAVVYVIAI 579

RESULT 15  
US-08-348-143-1  
Sequence 1, Application US/08348143  
Patent No. 5506205  
GENERAL INFORMATION:

APPLICANT: TAJIMA, HISAO  
APPLICANT: KITAGAWA, KOICHIRO  
APPLICANT: OHNO, HIROYUKI  
APPLICANT: UENO, TOSHIO  
TITLE OF INVENTION: A No. 5506205el Polypeptide of Protein p140 and DNAs  
encoding it

NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS  
 STREET: 2100 Pennsylvania Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20037-3202  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/348,143  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: JP 315806/1993  
 FILING DATE: 24-NOV-1993  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)293-7060  
 TELEFAX: (202)293-7860  
 TELEX: 6491103  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 993 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORGANISM: rat  
 TISSUE TYPE: skeletal muscle myoblast  
 CELL LINE: L6  
 US-08-348-143-1

Query Match 61.0%; Score 1765.5; DB 1; Length 993;

Best Local Similarity 58.9%; Pred. No. 1.2e-146; Matches 336; Conservative 80; Mismatches 123; Indels 31; Gaps 6;

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 46 QVCNVESSONNNLRKFIIRRGARHIVEMKTSVSDCSSIPVSGCKEFTNLYYFAD 105  
 71 QVCNVESSONNNLRKFIIRRGARHIVEMKTSVSDCSSIPVSGCKEFTNLYYFAD 130  
 106 FDSATKTFPMNMEPVKVTIADSFSDVIGGRVAKINTEVRSFGPVSRSGFYLAQ 165  
 131 SDVASASSPFMMENPKYKVTIADSFSDVIGGRVAKINTEVRSFGPVSRSGFYLAQ 186  
 166 DYGCMSLIVRVRYRRCPRIIIONGAIPOETLSGAESTSLVAARGSCIANAEVDPPIKL 225  
 187 DQACMSLISVRAFYKRCASTAGFALFPELTGAEPTSLVIAAGTCIANAEVSVPLKL 246  
 226 YCNGDGEMLVPVIGCMKAGFEAVENGTCVRCGPGSTFKANOGDEACTHCPINSRTSEG 285  
 247 YCNGDGEMLVPVIGCMKAGFEAVENGTCVRCGPGSTFKANOGDEACTHCPINSRTSEG 306  
 286 ATNCVCRNGYRADLDLPDPCCTTIPSAPOAVISSVNETISIMLEWTPPRDSGREDLYN 345  
 307 ASICTCHNNFRADSDVADACTVPPSPRGVISVNETSLILEMSEPRDLDGGRDLYN 366  
 346 IICKSCGSGRGA-----CTRCGDNVQYAPROLGITEPRITISDLAHOYTEEIOAVNGV 400  
 367 VICKKCRSGSGAGPATCSRCDDNVEFEPRDLGTERVHSHLAHRTFEVQAVNGV 426  
 401 TDOSPSPSPASVNTTQOAPSAVSIMHQSRTVDSITLSMSQPDOPNGVILDELOY 460  
 427 SKSPLPPRIAVNITTQOAPSAVSIMHQSRTVDSITLSMSQPDOPNGVILDELOY 486

QY 461 EKELSEYNATAIKSPNTV--TGIKAGAIYFQVRAVYAGIGRYSKMTFQMTF-AEY 517  
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 QY 518 QTSIQEKPLIIGSSAGIVFLAVVIAI 547  
 DB 545 AAOIQEOLPLIVGSTVAGFVFMVVVIAL 574

Search completed: February 1, 2002, 09:56:30  
 Job time: 210 sec

Fri Feb 1 11:16:37 2002

us-09-378-759-11\_copy\_1\_547.rai

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 1, 2002, 09:59:42 : Search time 192.18 Seconds

(without alignments)  
790.292 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 3148936 segs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending Patents\_AA\_Main:\*

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21: /cgn2\_6/ptodata/2/paa/US09.COMB.pep:\*

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23: /cgn2\_6/ptodata/2/paa/US09.COMB.pep:\*

24: /cgn2\_6/ptodata/2/paa/US09.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2895	100.0	970	8	US-08-449-645-11
2	2895	100.0	970	11	US-08-702-367-11
3	2895	100.0	970	17	US-09-378-759-11
4	2870	99.1	994	6	US-08-235-407-2
5	2870	99.1	994	11	US-08-727-463-2
6	2870	99.1	994	11	US-08-727-463-2
7	2870	99.1	994	11	US-08-730-700-2
8	2870	99.1	994	11	US-08-730-700-2
9	2870	99.1	994	20	US-09-621-595-2

10	2078.5	71.8	990	15	US-09-194-755A-7	Sequence 7, App1
11	1976	68.3	1009	3	US-07-861-390D-6	Sequence 6, App1
12	1800.5	62.2	998	8	US-08-449-645-20	Sequence 20, App1
13	1800.5	62.2	998	11	US-08-702-367-20	Sequence 20, App1
14	1800.5	62.2	998	17	US-09-378-759-20	Sequence 20, App1
15	1799.5	62.2	1007	1	PCT-US01-03800A-2273	Sequence 2273, App
16	1799.5	62.2	999	24	US-60-201-702-1172	Sequence 172, App
17	1789.5	61.8	961	24	US-60-200-366-202	Sequence 202, App
18	1789.5	61.8	961	24	US-60-201-702-165	Sequence 165, App
19	1765.5	61.0	993	19	US-09-558-340-1	Sequence 1, App1
20	1753	60.6	559	24	US-60-206-106-122	Sequence 122, App
21	1743.5	60.2	951	24	US-60-205-421-278	Sequence 278, App
22	1728.5	59.7	954	24	US-60-205-421-275	Sequence 275, App
23	1689.5	58.4	911	24	US-60-201-702-173	Sequence 6, App1
24	1687.5	58.3	1002	15	US-09-194-755A-6	Sequence 21, App
25	1671	57.7	908	24	US-60-200-366-211	Sequence 161, App
26	1671	57.7	908	24	US-60-201-702-161	Sequence 162, App
27	1614	55.8	947	24	US-60-201-702-161	Sequence 161, App
28	1582	54.6	905	24	US-60-205-421-289	Sequence 289, App
29	1580	54.6	889	24	US-60-205-421-289	Sequence 162, App
30	1485.5	51.3	993	21	US-09-751-389-7	Sequence 7, App1
31	1485.5	51.3	967	17	US-09-378-759-13	Sequence 8, App1
32	1485.5	51.3	975	21	US-09-378-759-30	Sequence 13, App1
33	1485.5	51.3	991	8	US-08-449-645-13	Sequence 13, App1
34	1485.5	51.3	991	11	US-08-702-367-13	Sequence 13, App1
35	1485.5	51.3	991	17	US-09-378-759-13	Sequence 13, App1
36	1485.5	51.3	991	22	US-09-823-187-14	Sequence 136, App
37	1482.5	51.2	666	21	US-09-771-161A-136	Sequence 3, App1
38	1482.5	51.2	983	1	PCT-US00-04326-5	Sequence 227, App
39	1482.5	51.2	983	21	US-09-771-161A-136	Sequence 103, App
40	1482.5	51.2	983	21	PCT-US00-04326-5	Sequence 6, App1
41	1482.5	51.2	983	21	US-09-771-161A-136	Sequence 21, App1
42	1481	51.2	1005	5	US-08-144-992-103	Sequence 21, App1
43	1478.5	51.1	968	8	US-09-751-389-6	Sequence 21, App1
44	1476.5	51.0	983	21	US-08-449-645-21	Sequence 21, App1
45	1476.5	51.0	983	11	US-08-702-367-21	Sequence 21, App1

#### ALIGNMENTS

RESULT 1

US-08-449-645-11

Sequence 11, Application US/08449645

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

APPLICANT: Welch, Andrew A.

APPLICANT: Jiny, Shuguan

TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESS: Amgen Patent Operations/RBW

STREET: 1840 Dehaviiland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,645

FILING DATE: May 24, 1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287-A

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 970 amino acids

TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-449-645-11

Query Match 100.0%; Score 2895; DB 8; Length 970;  
 Best Local Similarity 100.0%; Pred. No. 2,5e-261;  
 Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 LLAAVEETLMDSTTATATAGLGMVHPPSGMEVSGYDENMNTIRTYQVCNVESSQNNMLR 60
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DB 61 TFFIRRRGAHRIHVEKMFVSDCSIPSPGCKETFNLYYEADPDSATKTPNNMNEP 120
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DB 121 WKVVDITADESFSQVDLGGRYMKINTEVRSFGVSRSGFYLAFOYGGCMLIAVRVY 180
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DB 181 RKCPRITONGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDEMLVPIGRC 240
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OY 361 CGDNVOYAPROLGITEPRITYISDLAHTQYTFEIOAVNGVTDSPSPQFASVNTTNOA 420
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DB 361 CGDNVOYAPROLGITEPRITYISDLAHTQYTFEIOAVNGVTDSPSPQFASVNTTNOA 420
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DB 481 GLKAGAIYVQVARTVAGYGRYSGRMVFQMTAEAYQTSIOEKPLIIGSSAAGLVFLI 540
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DB 541 AVVVIAI 547

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RESULT 2  
 US-08-702-367-11  
 : Sequence 11, Application US/08702367  
 : GENERAL INFORMATION:  
 : APPLICANT: Fox, Gary M.  
 : TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
 : NUMBER OF INVENTION: Kinases  
 : NUMBER OF SEQUENCES: 28  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Amgen Patent Operations/RBW  
 : STREET: 1840 Dehavilland Drive  
 : CITY: Thousand Oaks  
 : STATE: California  
 : COUNTRY: USA  
 : ZIP: 91320  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/702,367

FILING DATE: 435  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/229,509  
 FILING DATE: 15-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE/DOCKET NUMBER: A-287  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 970 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-702-367-11

Query Match 100.0%; Score 2895; DB 11; Length 970;  
 Best Local Similarity 100.0%; Pred. No. 2,5e-261;  
 Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 TFFIRRRGAHRIHVEKMFVSDCSIPSPGCKETFNLYYEADPDSATKTPNNMNEP 120
OY 121 WKVVDITADESFSQVDLGGRYMKINTEVRSFGVSRSGFYLAFOYGGCMLIAVRVY 180
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DB 121 WKVVDITADESFSQVDLGGRYMKINTEVRSFGVSRSGFYLAFOYGGCMLIAVRVY 180
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DB 241 MCKAGFEAVENGTVRCGSPGTFKANOGEACTHCPINSRTTSEGAATNCVCRNGYRADL 300
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DB 481 GLKAGAIYVQVARTVAGYGRYSGRMVFQMTAEAYQTSIOEKPLIIGSSAAGLVFLI 540
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RESULT 3  
 US-09-378-759-11  
 : Sequence 11, Application US/09378759  
 : GENERAL INFORMATION:  
 : APPLICANT: Fox, Gary M.  
 : TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
 : NUMBER OF INVENTION: Kinases  
 : NUMBER OF SEQUENCES: 43  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Amgen Patent Operations/RBW  
 : STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: US/09/378,759  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,367  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 970 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-378-759-11

Query Match 100.0%; Score 2895; DB 17; Length 970;  
Best Local Similarity 100.0%; Pred. No. 2.5e-261;  
Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLAVEETLMDSTATAELGMMVHPSPGMEVSGYDENMNTIRTYOVYCNVFESSQNNMLR 60  
DB 1 LLAVEETLMDSTATAELGMMVHPSPGMEVSGYDENMNTIRTYOVYCNVFESSQNNMLR 60  
QY 61 TKFTRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYEADDSATKTPNNMEMP 120  
DB 61 TKFTRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYEADDSATKTPNNMEMP 120  
QY 121 WVKVDTLAADSFSQVDLGRVVKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 180  
DB 121 WVKVDTLAADSFSQVDLGRVVKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 180  
QY 181 RKPRIIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGMVLPIGRG 240  
DB 181 RKPRIIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGMVLPIGRG 240  
QY 241 MCKAGFAVENGTVRCGSPGTFKANGDEACTHCPINSRTTSEGATNCVCRNGYRADL 300  
DB 241 MCKAGFAVENGTVRCGSPGTFKANGDEACTHCPINSRTTSEGATNCVCRNGYRADL 300  
QY 301 DPLDMPTTIPSAPOAVISSVNETSLMLEWTPRDSGREDLVYNIICKSGSGRACR 360  
DB 301 DPLDMPTTIPSAPOAVISSVNETSLMLEWTPRDSGREDLVYNIICKSGSGRACR 360  
QY 361 CGDNVOYAPROQLTEPRYISDLAHTQYTFEIQAVNGVTOOSPPSPFAVNTTNA 420  
DB 361 CGDNVOYAPROQLTEPRYISDLAHTQYTFEIQAVNGVTOOSPPSPFAVNTTNA 420  
QY 421 APSAVSIMOVSTVSTVSLMSQDPQNGVILDELOYEKELESEYNTATIKSPNTVT 480  
DB 421 APSAVSIMOVSTVSTVSLMSQDPQNGVILDELOYEKELESEYNTATIKSPNTVT 480  
QY 481 GLKAGAIYFOVARTVAGYGRYSKMYFQMTAEYOTSIOEKPLITIGSSAAVLVLI 540  
DB 481 GLKAGAIYFOVARTVAGYGRYSKMYFQMTAEYOTSIOEKPLITIGSSAAVLVLI 540  
QY 541 AAVYVIAI 547  
DB 541 AAVYVIAI 547

RESULT 4  
US-08-235-407-2  
Sequence 2, Application US/08235407

GENERAL INFORMATION:  
APPLICANT: Pawson, Anthony  
APPLICANT: Henkemeyer, Mark  
TITLE OF INVENTION: NOVEL NEURAL KINASE AND RECEPTOR  
TITLE OF INVENTION: TYROSINE KINASE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bereskin & Parr  
STREET: 40 King Street West, Box 401  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 3Y2

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/235,407  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Kurd/dyk, Linda M  
REGISTRATION NUMBER: 34,971  
REFERENCE/DOCKET NUMBER: 3153-82  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 364-7311  
TELEFAX: (416) 361-1398

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 994 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Mus musculus  
DEVELOPMENTAL STAGE: Embryo  
IMMEDIATE SOURCE:  
LIBRARY: lambda gt10 cDNA library  
CLONE: Combined pNKRACE A2 and K2 and cDNA clones  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: Distal end of chromosome 4  
MAP POSITION: near the ahd-1 mutation  
US-08-235-407-2

Query Match 99.1%; Score 2870; DB 6; Length 994;  
Best Local Similarity 98.9%; Pred. No. 5.7e-259;  
Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

QY 1 LLAVEETLMDSTATAELGMMVHPSPGMEVSGYDENMNTIRTYOVYCNVFESSQNNMLR 60  
DB 23 LLAVEETLMDSTATAELGMMVHPSPGMEVSGYDENMNTIRTYOVYCNVFESSQNNMLR 82  
QY 61 TKFTRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYEADDSATKTPNNMEMP 120  
DB 61 TKFTRRGARHRIHEMKFSVRDCSSIPVSGCKETFNLYYEADDSATKTPNNMEMP 142  
QY 121 WVKVDTLAADSFSQVDLGRVVKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 180  
DB 143 WVKVDTLAADSFSQVDLGRVVKINTEVRSFGPVSRSGFYLAFOYGGCMLIAVRVY 202  
QY 181 RKPRIIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGMVLPIGRG 240  
DB 203 RKPRIIONGAIFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGMVLPIGRG 262

```

QY 241 MCKAGFEAVENGTCRCGPGSTFRKANGDEACTHCPINSRTSGATNCYCRNGYRADL 300
Db 263 MCKAGFEAVENGTCRCGPGSTFRKANGDEACTHCPINSRTSGATNCYCRNGYRADL 322
QY 301 DPLMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 360
Db 323 DPLMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 382
QY 361 CGDNVQVAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPFSQFASVNTTNOA 420
Db 383 CGDNVQVAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPFSQFASVNTTNOA 442
QY 421 APSAVSIMHOVSRTVDSITLMSQPDQPNVILDELYEKELESEYNATAIKSPNTVT 480
Db 443 APSAVSIMHOVSRTVDSITLMSQPDQPNVILDELYEKELESEYNATAIKSPNTVT 502
QY 481 --GLKAGAIYFQVBARVYAGRGSKMYQTMTAEAYOTSIQKELPLIGSSAAGLVF 538
Db 503 VQGLKAGAIYFQVBARVYAGRGSKMYQTMTAEAYOTSIQKELPLIGSSAAGLVF 562
QY 539 LIAVVVIAI 547
Db 563 LIAVVVIAI 571

```

## RESULT 5

```

US-08-727-463-2
; Sequence 2, Application us/08727463

```

## GENERAL INFORMATION:

```

APPLICANT: PAMSON, Anthony
APPLICANT: Henkemeyer, Mark
APPLICANT: Letwin, Kenneth
TITLE OF INVENTION: NEURAL RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: MERCHANT & GOULD
STREET: 3100 Northwest Center, 90 South Seventh Street
CITY: Minneapolis
STATE: Minnesota
COUNTRY: U.S.A.
ZIP: 55403-4131

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## COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,463
FILING DATE: 18-OCT-1996
CLASSIFICATION: 800

```

## ATTORNEY/AGENT INFORMATION:

```

NAME: Mueller, Douglas P.
REGISTRATION NUMBER: 30,300
REFERENCE/DOCKET NUMBER: M&G 7933.89-US-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 332-5300
TELEFAX: (612) 332-9081

```

## INFORMATION FOR SEQ ID NO: 2:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Mus musculus
DEVELOPMENTAL STAGE: Embryo
IMMEDIATE SOURCE:
LIBRARY: lambda gt10 cDNA library
CLONE: Combined pNURACE A2 and K2 and cDNA clones
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Distal end of chromosome 4
MAP POSITION: near the ahd-1 mutation

```

US-08-727-463-2

```

Query Match          99.1%; Score 2870; DB 11; Length 994;
Best local Similarity 98.9%; Pred. No. 5,7e-259;
Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

```

```

QY 1 LLAVESTLMDSTTATAEALGMMVHPSPGMEVEVSGYDENNTIRTYOVAVFESSQNNMLR 60
Db 23 LLAVESTLMDSTTATAEALGMMVHPSPGMEVEVSGYDENNTIRTYOVAVFESSQNNMLR 82
QY 61 TKFIRRGARHRIHVEKMFVYRDCSSIPVPGCKEFTFNLYYHADPDSATKTFPMNMEHP 120
Db 83 TKFIRRGARHRIHVEKMFVYRDCSSIPVPGCKEFTFNLYYHADPDLATKTFPMNMEHP 142
QY 121 WVKYDTIAADESFQVDLGGRVKMKINTEVSRFGVRSRGFYLAFOYGGCMSLIAVRVY 180
Db 143 WVKYDTIAADESFQVDLGGRVKMKINTEVSRFGVRSRGFYLAFOYGGCMSLIAVRVY 202
QY 181 RKCPRIIONGAIFQETLSGAESTSLVARSGCIANAEVDVPIKLYCNGDEMLVPIGRG 240
Db 203 RKCPRIIONGAIFQETLSGAESTSLVARSGCIANAEVDVPIKLYCNGDEMLVPIGRG 262
QY 241 MCKAGFEAVENGTCRCGPGSTFRKANGDEACTHCPINSRTSGATNCYCRNGYRADL 300
Db 263 MCKAGFEAVENGTCRCGPGSTFRKANGDEACTHCPINSRTSGATNCYCRNGYRADL 322
QY 301 DPLMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 360
Db 323 DPLMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 382
QY 361 CGDNVQVAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPFSQFASVNTTNOA 420
Db 383 CGDNVQVAPROLGLTEPRITYISDLAHTQYTFEIOAVNGVTDOSPFSQFASVNTTNOA 442
QY 421 APSAVSIMHOVSRTVDSITLMSQPDQPNVILDELYEKELESEYNATAIKSPNTVT 480
Db 443 APSAVSIMHOVSRTVDSITLMSQPDQPNVILDELYEKELESEYNATAIKSPNTVT 502
QY 481 --GLKAGAIYFQVBARVYAGRGSKMYQTMTAEAYOTSIQKELPLIGSSAAGLVF 538
Db 503 VQGLKAGAIYFQVBARVYAGRGSKMYQTMTAEAYOTSIQKELPLIGSSAAGLVF 562
QY 539 LIAVVVIAI 547
Db 563 LIAVVVIAI 571

```

## RESULT 6

```

US-08-727-463-2
; Sequence 2, Application us/08727463A

```

## GENERAL INFORMATION:

```

APPLICANT: PAMSON, ANTHONY
APPLICANT: HENKEMEYER, MARK
APPLICANT: LETWIN, KENNETH
APPLICANT: MOUNT SINAI HOSPITAL CORPORATION
TITLE OF INVENTION: METHODS FOR IDENTIFYING SUBSTANCES AFFECTING RECEPTOR
TITLE OF INVENTION: TYROSINE KINASE ACTIVITY (AS AMENDED)
FILE REFERENCE: 7933.89USWO
CURRENT APPLICATION NUMBER: US/08/727,463A
CURRENT FILING DATE: 1997-03-11
EARLIER APPLICATION NUMBER: PCT/CA95/00254
EARLIER FILING DATE: 1995-04-28
EARLIER APPLICATION NUMBER: 08/235,407
EARLIER FILING DATE: 1994-04-29

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## NUMBER OF SEQ ID NOS: 4

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 994
TYPE: PRT
ORGANISM: Mus musculus
US-08-727-463-2

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Query Match 99.1%; Score 2870; DB 11; Length 994;  
 Best Local Similarity 98.9%; Pred. No. 5.7e-259;  
 Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

```

OY 1 LLAAVETLMDSTTATTAELGMMVHPSPGMEVSGYDENNTIRTYOVCFESSQNNMLR 60
DB 23 LLAAVETLMDSTTATTAELGMMVHPSPGMEVSGYDENNTIRTYOVCFESSQNNMLR 82
OY 61 TKFIRRGARHRIHVEKFSVRDCCSIPVSGCKETFNLYYYEADFDLATKTFPMNMENP 120
DB 83 TKFIRRGARHRIHVEKFSVRDCCSIPVSGCKETFNLYYYEADFDLATKTFPMNMENP 142
OY 121 WVKVDTIADESFQVDLGRVAKINTEVRSFGVSRSGFYLAFODYGCMSLIAVRVY 180
DB 143 WVKVDTIADESFQVDLGRVAKINTEVRSFGVSRSGFYLAFODYGCMSLIAVRVY 202
OY 181 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPILKLYCNGDEMLVPIGR 240
DB 203 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPILKLYCNGDEMLVPIGR 262
OY 241 MCKAGEAVENGTCRGCPSTGTFKANOGEACTHCPINSRTTSGATNCVCNRYRADL 300
DB 263 MCKAGEAVENGTCRGCPSTGTFKANOGEACTHCPINSRTTSGATNCVCNRYRADL 322
OY 301 DPLDMCTTIPAPQAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
DB 323 DPLDMCTTIPAPQAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 382
OY 361 CGDNVOYARQGLTEPRITISDLAHTOYFETIOAVNGVTDOSPFSPQASVNTITNOA 420
DB 383 CGDNVOYARQGLTEPRITISDLAHTOYFETIOAVNGVTDOSPFSPQASVNTITNOA 442
OY 421 APSAVSIHQVSRVYDSTLTSMSOPDPQNGVILDELOYYEKELSEYNATAIKSPNTVT 480
DB 443 APSAVSIHQVSRVYDSTLTSMSOPDPQNGVILDELOYYEKELSEYNATAIKSPNTVT 502
OY 481 --GLKAGAIYFOVRAVAGYGRYSKMYFOTMTAEYOTSIOEKPLTIGSSAGLVF 538
DB 503 VQGLKAGAIYFOVRAVAGYGRYSKMYFOTMTAEYOTSIOEKPLTIGSSAGLVF 562
OY 539 LIAVVYIAI 547
DB 563 LIAVVYIAI 571

```

# RESULT 7

US-08-730-700-2  
 ; Sequence 2, Application US/08730700  
 ; GENERAL INFORMATION:

APPLICANT: Pawson, Anthony  
 TITLE OF INVENTION: Method of Activating a Novel Ligand  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Bereskin & Parr  
 STREET: 40 King Street West, Box 401  
 CITY: Toronto

STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5H 3Y2

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/730,700

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kurdydk, Linda M.

REGISTRATION NUMBER: 34,971  
 REFERENCE/DOCKET NUMBER: 3153-197  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 364-7311  
 TELEFAX: (416) 361-1398  
 TELEX: 06-23115

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 994 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: Mus musculus

DEVELOPMENTAL STAGE: Embryo

IMMEDIATE SOURCE:

LIBRARY: lambda gt10 cDNA library

CLONE: Combined pNURACE A2 and K2 and cDNA clones

POSITION IN GENOME:

CHROMOSOME/SEGMENT: Distal end of chromosome 4

MAP POSITION: near the and-1 mutation

US-08-730-700-2

Query Match 99.1%; Score 2870; DB 11; Length 994;  
 Best Local Similarity 98.9%; Pred. No. 5.7e-259;  
 Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

```

OY 1 LLAAVETLMDSTTATTAELGMMVHPSPGMEVSGYDENNTIRTYOVCFESSQNNMLR 60
DB 23 LLAAVETLMDSTTATTAELGMMVHPSPGMEVSGYDENNTIRTYOVCFESSQNNMLR 82
OY 61 TKFIRRGARHRIHVEKFSVRDCCSIPVSGCKETFNLYYYEADFDLATKTFPMNMENP 120
DB 83 TKFIRRGARHRIHVEKFSVRDCCSIPVSGCKETFNLYYYEADFDLATKTFPMNMENP 142
OY 121 WVKVDTIADESFQVDLGRVAKINTEVRSFGVSRSGFYLAFODYGCMSLIAVRVY 180
DB 143 WVKVDTIADESFQVDLGRVAKINTEVRSFGVSRSGFYLAFODYGCMSLIAVRVY 202
OY 181 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPILKLYCNGDEMLVPIGR 240
DB 203 RKCPRITONGALFOETLSGAESTSLVAARGSCIANAEVDVPILKLYCNGDEMLVPIGR 262
OY 241 MCKAGEAVENGTCRGCPSTGTFKANOGEACTHCPINSRTTSGATNCVCNRYRADL 300
DB 263 MCKAGEAVENGTCRGCPSTGTFKANOGEACTHCPINSRTTSGATNCVCNRYRADL 322
OY 301 DPLDMCTTIPAPQAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 360
DB 323 DPLDMCTTIPAPQAVISSVNETSLMEWTPPRDSGREDLVYNIICKSGSGRGACTR 382
OY 361 CGDNVOYARQGLTEPRITISDLAHTOYFETIOAVNGVTDOSPFSPQASVNTITNOA 420
DB 383 CGDNVOYARQGLTEPRITISDLAHTOYFETIOAVNGVTDOSPFSPQASVNTITNOA 442
OY 421 APSAVSIHQVSRVYDSTLTSMSOPDPQNGVILDELOYYEKELSEYNATAIKSPNTVT 480
DB 443 APSAVSIHQVSRVYDSTLTSMSOPDPQNGVILDELOYYEKELSEYNATAIKSPNTVT 502
OY 481 --GLKAGAIYFOVRAVAGYGRYSKMYFOTMTAEYOTSIOEKPLTIGSSAGLVF 538
DB 503 VQGLKAGAIYFOVRAVAGYGRYSKMYFOTMTAEYOTSIOEKPLTIGSSAGLVF 562
OY 539 LIAVVYIAI 547
DB 563 LIAVVYIAI 571

```

# RESULT 8

US-08-730-700A-2  
 ; Sequence 2, Application US/08730700A

GENERAL INFORMATION:  
APPLICANT: Pawson, Anthony  
TITLE OF INVENTION: Method of Activating a Novel Ligand  
TITLE OF INVENTION: Regulatory Pathway  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Room 970  
STREET: 600 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1X5  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/730,700A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,518  
FILING DATE: 13-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kurdydyk, Linda M.  
REGISTRATION NUMBER: 34,971  
REFERENCE/DOCKET NUMBER: 3153-196  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 416-586-3235  
TELEFAX: 416-586-3110  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 994 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-730-700A-2

Query Match 99.1%; Score 2870; DB 11; Length 994;  
Best Local Similarity 98.9%; Pred. No. 5.7e-259;  
Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

1 LLAVEETLMDSTATAELGMVHPSPGMEVSGYDENMNTIRTYOVCHVFESSQNNMLR 60  
23 LLAVEETLMDSTATAELGMVHPSPGMEVSGYDENMNTIRTYOVCHVFESSQNNMLR 82  
61 TKFTRRGARHRIHEMKFSYVDCSSIPVSGCKETFNLYYEADPDSATKTFPNNMNP 120  
83 TKFTRRGARHRIHEMKFSYVDCSSIPVSGCKETFNLYYEADPDLATKTFPNNMNP 142  
121 WKVDTLADSFQVLDGGRVMIINTEVRSFGVSRSGFYLAFODYGGCMLIAVVFY 180  
143 WKVDTLADSFQVLDGGRVMIINTEVRSFGVSRSGFYLAFODYGGCMLIAVVFY 202  
181 RKCPRIIONGALFDETLTSGAESTSLVAARGSCINAAEEVDVPIKLYCNGDEMLVPIGR 240  
203 RKCPRIIONGALFDETLTSGAESTSLVAARGSCINAAEEVDVPIKLYCNGDEMLVPIGR 262  
241 MKAFFEVENGTGRCGPGSGTFKANGDEACTHCPINRSTTSEGATNCVCRNGYRADL 300  
263 MKAFFEVENGTGRCGPGSGTFKANGDEACTHCPINRSTTSEGATNCVCRNGYRADL 322  
301 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGREDLVYNIICKSGSGGACTR 360  
323 DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGREDLVYNIICKSGSGGACTR 382  
361 CGDNVOYAROLGTEPRITISDLAHTOYTFEIOAVNGVTDQSPFQFASVNTITNOA 420  
383 CGDNVOYAROLGTEPRITISDLAHTOYTFEIOAVNGVTDQSPFQFASVNTITNOA 442

421 APSAVSIMHOVSRTVDSTLMSOPDPONGVILDELOYEKEISEYNATAIKSPNTVT 480  
443 APSAVSIMHOVSRTVDSTLMSOPDPONGVILDELOYEKEISEYNATAIKSPNTVT 502  
481 --GLKAGAIYVQVARFVAGYGRYSGKMYFQTMTEAEYQISQIEKPLIIGSSAGIYF 538  
503 VQGLKAGAIYVQVARFVAGYGRYSGKMYFQTMTEAEYQISQIEKPLIIGSSAGIYF 562  
539 LIAVVVIAI 547  
563 LIAVVVIAI 571

RESULT 9  
US-09-621-595-2  
Sequence 2, Application US/09621595  
GENERAL INFORMATION:  
APPLICANT: Pawson, Anthony  
TITLE OF INVENTION: Method of Activating a Novel Ligand  
TITLE OF INVENTION: Regulatory Pathway  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Room 970  
STREET: 600 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5G 1X5  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/621,595  
FILING DATE: 21-Jul-2000  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/730,700  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Kurdydyk, Linda M.  
REGISTRATION NUMBER: 34,971  
REFERENCE/DOCKET NUMBER: 3153-196  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 416-586-3235  
TELEFAX: 416-586-3110  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 994 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-621-595-2

Query Match 99.1%; Score 2870; DB 20; Length 994;  
Best Local Similarity 98.9%; Pred. No. 5.7e-259;  
Matches 543; Conservative 3; Mismatches 1; Indels 2; Gaps 1;

1 LLAVEETLMDSTATAELGMVHPSPGMEVSGYDENMNTIRTYOVCHVFESSQNNMLR 60  
23 LLAVEETLMDSTATAELGMVHPSPGMEVSGYDENMNTIRTYOVCHVFESSQNNMLR 82  
61 TKFTRRGARHRIHEMKFSYVDCSSIPVSGCKETFNLYYEADPDSATKTFPNNMNP 120  
83 TKFTRRGARHRIHEMKFSYVDCSSIPVSGCKETFNLYYEADPDLATKTFPNNMNP 142  
121 WKVDTLADSFQVLDGGRVMIINTEVRSFGVSRSGFYLAFODYGGCMLIAVVFY 180

```

Db 143 WKVVTIADESESQVDLGGVRVAKINTFEVRSGPVSRNGFYLAFODYGCMSLIAVRFY 202
OY 181 RKCPRIONGAIFOEITLGAESTSLVAARGSCITANAEEVDVPIKLYCNGDGMVLPIGR 240
Db 203 RKCPRIONGALFOETLSGAESTSLVAARGSCITANAEEVDVPIKLYCNGDGMVLPIGR 262
OY 241 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSEGATNCVCRNGYRADL 300
Db 263 MCKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSEGATNCVCRNGYRADL 322
OY 301 DPLDMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDGGREDLVYITICKSGSGGACTR 360
Db 323 DPLDMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDGGREDLVYITICKSGSGGACTR 382
OY 361 CGDNQVAPROLGLEPRITISDLAHTQYFEIOAVNGVTDOSPSPOPASVNTTMOA 420
Db 383 CGDNQVAPROLGLEPRITISDLAHTQYFEIOAVNGVTDOSPSPOPASVNTTMOA 442
OY 421 APSAVSIMHOVSRTVDSITLSMSQPDQPNVILDELOYEKELESEYNATAIKSPTNTVT 480
Db 443 APSAVSIMHOVSRTVDSITLSMSQPDQPNVILDELOYEKELESEYNATAIKSPTNTVT 502
OY 481 --GLKAGAIYFOVARARVAGYGRSGKMYFOTMTEAEYQTSIQKLEPLITIGSSAGLVF 538
Db 503 VOGLAGAIYFOVARARVAGYGRSGKMYFOTMTEAEYQTSIQKLEPLITIGSSAGLVF 562
OY 539 LIAVVVIAI 547
Db 563 LIAVVVIAI 571

RESULT 10
US-09-194-755A-7
: Sequence 7, Application US/09194755A
: GENERAL INFORMATION:
: APPLICANT: Matsui, Toshimitsu
: TITLE OF INVENTION: Novel Human Receptor Type Tyrosine
: TITLE OF INVENTION: Kinases Like Protein
: FILE REFERENCE: 07541.0001-00000
: CURRENT APPLICATION NUMBER: US/09/194,755A
: PRIOR FILING DATE: 1999-04-14
: PRIOR APPLICATION NUMBER: PCT/JP97/01887
: PRIOR FILING DATE: 1997-06-04
: PRIOR APPLICATION NUMBER: JP 141849/1996
: PRIOR FILING DATE: 1996-06-04
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 7
: LENGTH: 990
: TYPE: PRT
: ORGANISM: Rattus sp.
US-09-194-755A-7

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```

Query Match 71.8%; Score 2078.5; DB 15; Length 990;
Best Local Similarity 67.9%; Pred. No. 8,7e-185;
Matches 376; Conservative 86; Mismatches 83; Indels 9; Gaps 3;

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OY 2 LAAVEETLMDSTTATLGLMVMVHP-PSGMEVSGYDENMNTIRTYOVNVESSONNLRT 61
Db 15 VAAHEETLMDTTRTATLGLTANPASWHEEYSGIDENLNTIRTYOVNVEEPNONNLRT 74
OY 62 KFIIRRGAAHRIHWEKFSVBDSCSIPSPGSKETENLYYYEADFDSATKTFPMENPM 121
Db 75 TFIIRRGAAHRIYTEMRTVDCSLPVPSPGSKETENLYYYEADFSATKTKSAFWMSAPY 134
OY 122 VKYDTIAADSEFS-----QVDLGGVRVAKINTFEVRSGPVSRNGFYLAFODYGCMSLIA 175
Db 135 LKVDYTIADSEFSSSSAAMQVDFGGRMLKVNTVEYRSGPLTRNGFYLAFODYGACMSILS 194
OY 176 VRFVYRKCPRIONGAIFOEITLGAESTSLVAARGSCITANAEEVDVPIKLYCNGDGMVL 235

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Db 195 VRFVYRKCPRIONGAIFOEITLGAESTSLVIARTCTIPNAEEVDVPIKLYCNGDGMVL 254
OY 236 PIGRCMKAGFEAVENGTCVRCGPGSGTFKANOGEDEACTHCPINSRTTSEGATNCVCRNGY 295
Db 255 PIGRCMKAGYEP-ENSVACACAPAGTFKASQEAEGSCHPSNSRSPSEAPICTCRGY 313
OY 296 YRADLDPLEDMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDGGREDLVYITICKSGSGR 355
Db 314 YRADLDPLEDMPCCTTIPSAPOAVISSVNETSLMLEWTPPRDGGREDLVYITICKSGSGR 373
OY 356 GACTRCGDNQVAPROLGLEPRITISDLAHTQYFEIOAVNGVTDOSPSPOPASVNI 415
Db 374 RSCRCDDNVFVFOVROLGLEPRITISDLAHTQYFEIOAVNGVTDOSPSPOPASVNI 433
OY 416 TTNOAASVAVSIMHOVSRTVDSITLSMSQPDQPNVILDELOYEKELESEYNATAIKSP 475
Db 434 TTNOAASVAVSIMHOVSRTVDSITLSMSQPDQPNVILDELOYEKELESEYNATAIKSP 493
OY 476 TNT--VTGLKAGAIYFOVARARVAGYGRSGKMYFOTMTEAEYQTSIQKLEPLITIGSSA 533
Db 494 TNTARIDGLRGMYVVOVARARVAGYGRSGKMYFOTMTEAEYQTSIQKLEPLITIGSSA 553
OY 534 AGVFEVVSIVAISI 547
Db 554 AGVFEVVSIVAISI 567

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RESULT 11
US-07-861-390D-6
: Sequence 6, Application US/07861390D
: GENERAL INFORMATION:
: APPLICANT: PAMSON et al.
: TITLE OF INVENTION: METHOD FOR EXPRESSING A
: TITLE OF INVENTION: PHOSPHORYLATED PROTEIN
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Linda M. Kurdzyk, Bereskin & Parr
: STREET: 40 King Street West, P. O. Box 401
: CITY: Toronto, Ontario
: STATE: N/A
: COUNTRY: Canada
: ZIP: M5H 3Y2
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: DOS Text File
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/861,390D
: FILING DATE: 19920331
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: J.G. Mullins
: REGISTRATION NUMBER: 33073
: REFERENCE/DOCKET NUMBER: 027-021
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 684-1111
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1009 amino acids
: TYPE: AMINO ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-07-861-390D-6

```

```

Query Match 68.3%; Score 1976; DB 3; Length 1009;
Best Local Similarity 66.0%; Pred. No. 3,6e-175;
Matches 371; Conservative 86; Mismatches 89; Indels 16; Gaps 10;
OY 2 LAAVEETLMDSTTATLGLMVMVHP-PSGMEVSGYDENMNTIRTYOVNAV-PESSONNL 59

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Db 15 VAAMEETIMDTTRATATLGTWANTANPKASGMEVSGYDENLNTIRTYQVCNAXFEPNOMNL 74
OY 60 RTKTRRRG-AARIHVEKFSVRDCCSIPSV--GSKETENLYYEADFSATKTPBNW 116
Db 75 LTTFINRGKXAHRIYETKRFYVROCSSLPNVXXGSKCKETFLYETDVIATKKSAMW 134
OY 117 MENWVAVDTIADESFOVDLGRVAKINTEVRSFGVYSRGFLAODYGGCMLAV 176
Db 135 SEAPLKADYDIAADESFQVDFGRLMKVTEVRSFGLTRNGFLAODYGCACMSLLSY 194
OY 177 RVEYKRCRIIONGAIPEQETLSGASTSLVAARGSCIANAEVDVP---IKLYCGDGEW 233
Db 195 RVEFKKCSIYONFAVEFELMTGAESTSLVARGTCIPNAEVDVPPXXIKIKYCGDGEW 254
OY 234 LVPICRCMKAGFEAVENGTCRGCPSGTFKANOGDEACTHCPINSRTTSEGATNCVCBN 293
Db 255 MYPICRCCKAGFEAVENGTCRGCPSGTFKANOGDEACTHCPINSRTTSEGATNCVCBN 314
OY 294 GYRADLPDLMPCCTTISAPQAVISSV-NETSULEMTPPRDSGREDLVYNIICKSCG 352
Db 315 GYRADFPPEPACSVSPGPRNVISYXNETSILEMHPRETEGRODVTYNIICKSCX 374
OY 353 SGRG---ACTRCGDVNOYAPROLGLTEPRITYSDLAHTQYTFEIOAVNGVTDOSPFSPO 409
Db 375 XKRADRRSCSRODDNVEFPRDLGLECHVSISLMAHTPYTFDQALINGVSKSPFPQ 434
OY 410 -FASVNTTNOAPSAVSIMHO-VSRFYDSTILWSQDPQNGVILIDYLOYEKELSEY 467
Db 435 HVXSVNTTNOAPSTVPIHMOXVSATIMRSITLSPQPOPGIILDEIRIYEKEHNEF 494
OY 468 NATAIKSPNT--VTGLKGAIVYFOVARTAVAGRYSGKMYEOTMTEAEFOTSIQEL 525
Db 495 NSMARSOITNARIIDLGRGWYVVOVRAIRYAGIKCFSGKMGFOTLTDODDKSELREGL 554
OY 526 PLIGSSAAGVELLAVVIAI 547
Db 555 PLIAGSAGVVEVSLVAISI 576

RESULT 12
; Sequence 20, Application US/08449645
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; APPLICANT: Melcher, Andrew A.
; APPLICANT: Jung, Shuguan
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehaviiland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645
; FILING DATE: May 24, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287-A
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645-20

Query Match 62.2%; Score 1800.5; DB 8; Length 998;
Best Local Similarity 61.9%; Pred. No. 1e-158;
Matches 340; Conservative 79; Mismatches 119; Gaps 5;

OY 4 AVEETIMDTTRATATLGTWANTANPKASGMEVSGYDENLNTIRTYQVCNAXFEPNOMNL 63
Db 37 ALAETIMDTTRATATLGTWANTANPKASGMEVSGYDENLNTIRTYQVCNAXFEPNOMNL 96
OY 64 IRRGAHRIHVEKFSVRDCCSIPSV--GSKETENLYYEADFSATKTPBNW 123
Db 97 IMRWVAVDTIADESFOVDLGRVAKINTEVRSFGVYSRGFLAODYGGCMLAV 156
OY 124 VDTIADESFOVDLGRVAKINTEVRSFGVYSRGFLAODYGGCMLAV 183
Db 157 VDTIADESFOVDLGRVAKINTEVRSFGVYSRGFLAODYGGCMLAV 212
OY 184 PRIONGAIFQETLSGASTSLVAARGSCIANAEVDVPPIKLYCGDGEW 243
Db 213 ASTAGFALFPELTIGABEPTSLVAPGTCIPNAEVSYPKLYCGDGEW 272
OY 244 AGFEAVENGTCRGCPSGTFKANOGDEACTHCPINSRTTSEGATNCVCBN 303
Db 273 TGHFRAKESQCRPSPGSRKAKOGEGCLPCPNSRTTSPASICTCHNNFYRADSDSA 332
OY 304 DMCCTTISAPQAVISSV-NETSULEMTPPRDSGREDLVYNIICKSC--GSGRACRC 361
Db 333 DSACTTVSPRPGVSIHNETSLILEMHPRETEGRODVTYNIICKSC 392
OY 362 GNNVOYAPROLGLTEPRITYSDLAHTQYTFEIOAVNGVTDOSPFSAPVNTTNOA 421
Db 393 DNVEFPRDLGLECHVSISLMAHTPYTFDQALINGVSKSPFPQ 452
OY 422 PSASIMHOVSRFYDSTILWSQDPQNGVILIDYLOYEKELSEY 479
Db 453 PSEVPTLRHSSGSLTSMAPPERPENGVIIDYEKYEK--SGIASTVSONKNSVOL 510
OY 480 TELKAGAIYFOVARTAVAGRYSGKMYEOTMTE-AEYQTSIOELPLIIGSSAAGVEL 538
Db 511 DGLRPDARVVOVARTAVAGRYSGKMYEOTMTE-AEYQTSIOELPLIIGSSAAGVEL 570
OY 539 LIAVVIAI 547
Db 571 VVAVVIAI 579

RESULT 13
; Sequence 20, Application US/08702367
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; APPLICANT: Melcher, Andrew A.
; APPLICANT: Jung, Shuguan
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehaviiland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367
; FILING DATE:

```

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/229,509  
FILING DATE: 15-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 998 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-702-367-20

Query Match 62.2% Score 1800.5; DB 11; Length 998;  
Best Local Similarity 61.9%; Pred. No. 1e-158;  
Matches 340; Conservative 79; Mismatches 119; Indels 11; Gaps 5;

QY 4 AVEETLMDSTATAELGMVHPPSGMEVSGYDENMNTIRTYQVCNVPESSONMMLRTKF 63  
DB 37 ALEETLMDTKWTSSELAFTSHESGMEVSGYDENMNTIRTYQVCNVPESSONMMLRTKF 96  
QY 64 IRRGAHRIHVMKTSVDCSSIPSPGCKETNLYYYEADFSDATKTPNMENPVK 123  
DB 97 IMRDVORVYELKFTVDCNSIPNIPGCKETNLYYYEADFSDATKTPNMENPVK 156  
QY 124 VDTIADESFQVDLGGVYMKINTFVRSFGVRSGLAFADYDGGCMLAVAVFYKRC 183  
DB 157 VDTIAPDESFSRLDAG---RVNTRKVSFGPLSKAGFLAFQDQACMSLISVAFYKRC 212  
QY 184 PRIIONGAIFQETLSGASTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGRCK 243  
DB 213 ASTAGFALFPELTGAEPTSLVIAFGTCIPNAVEVSVPKLYCNGDGEMLVPIGRCK 272  
QY 244 AGFEAVENGTCVRCGPGSTGFANOGDEACTHCPTNSRTSGATNCVRCNGYRADLPL 303  
DB 273 TGEHPAAKESQCRCPSPSTYAKOGEGPCLPSPNSRTSPAAISICCHNNFYRADSDA 332  
QY 304 DMCPTTIPSAQVAIVSSVNETSLMLEWTPPRDSGREDLVYNIICKSC--GSGRGACTRC 361  
DB 333 DSACTVPSPPRGVSNVNETSLILEMSEPRDLGVRDLLXNYICKCHGAGGASACSRC 392  
QY 362 GDNVOYAPROLGLTEPRYISDLAHTQYTFEIOAVNGVTDOSPFSPQFASVNTTNOAA 421  
DB 393 DDNEVFYRQGLSEPRVHTSHLAHRTYFEVOAVNGVSGKSPLPYRAVAVNTTNOAA 452  
QY 422 PSASIMHOVSRTVDSITLSMSOPDOPNGVILDELOYEKEISEYNATAIKSPNTV-- 479  
DB 453 PSEVPTLRHLSSSSSLTLSWAPERNGVILDEYEMKFEK--SEGIASTVYTSOMNSVOL 510  
QY 480 TGLKAGLIYVOVARVAVAGYGRYSGKMYFQMTF--AEYTSIOEKPLITIGSSAGLVF 538  
DB 511 DGLRPDARIYVOVARVAVAGYGRYSGKMYFQMTF--AEYTSIOEKPLITIGSSAGLVF 570  
QY 539 LIAVVYIAI 547  
DB 571 VVAVVYIAI 579

RESULT 14  
US-09-378-759-20  
Sequence 20, Application US/09378759  
GENERAL INFORMATION:  
APPLICANT: Fox, Gary M.  
TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
TITLE OF INVENTION: Kinases  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Patent Operations/RBW  
STREET: 1840 Dehavenland Drive

CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,759  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,367  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-287  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 998 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-378-759-20

Query Match 62.2% Score 1800.5; DB 17; Length 998;  
Best Local Similarity 61.9%; Pred. No. 1e-158;  
Matches 340; Conservative 79; Mismatches 119; Indels 11; Gaps 5;

QY 4 AVEETLMDSTATAELGMVHPPSGMEVSGYDENMNTIRTYQVCNVPESSONMMLRTKF 63  
DB 37 ALEETLMDTKWTSSELAFTSHESGMEVSGYDENMNTIRTYQVCNVPESSONMMLRTKF 96  
QY 64 IRRGAHRIHVMKTSVDCSSIPSPGCKETNLYYYEADFSDATKTPNMENPVK 123  
DB 97 IMRDVORVYELKFTVDCNSIPNIPGCKETNLYYYEADFSDATKTPNMENPVK 156  
QY 124 VDTIADESFQVDLGGVYMKINTFVRSFGVRSGLAFADYDGGCMLAVAVFYKRC 183  
DB 157 VDTIAPDESFSRLDAG---RVNTRKVSFGPLSKAGFLAFQDQACMSLISVAFYKRC 212  
QY 184 PRIIONGAIFQETLSGASTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGRCK 243  
DB 213 ASTAGFALFPELTGAEPTSLVIAFGTCIPNAVEVSVPKLYCNGDGEMLVPIGRCK 272  
QY 244 AGFEAVENGTCVRCGPGSTGFANOGDEACTHCPTNSRTSGATNCVRCNGYRADLPL 303  
DB 273 TGEHPAAKESQCRCPSPSTYAKOGEGPCLPSPNSRTSPAAISICCHNNFYRADSDA 332  
QY 304 DMCPTTIPSAQVAIVSSVNETSLMLEWTPPRDSGREDLVYNIICKSC--GSGRGACTRC 361  
DB 333 DSACTVPSPPRGVSNVNETSLILEMSEPRDLGVRDLLXNYICKCHGAGGASACSRC 392  
QY 362 GDNVOYAPROLGLTEPRYISDLAHTQYTFEIOAVNGVTDOSPFSPQFASVNTTNOAA 421  
DB 393 DDNEVFYRQGLSEPRVHTSHLAHRTYFEVOAVNGVSGKSPLPYRAVAVNTTNOAA 452  
QY 422 PSASIMHOVSRTVDSITLSMSOPDOPNGVILDELOYEKEISEYNATAIKSPNTV-- 479  
DB 453 PSEVPTLRHLSSSSSLTLSWAPERNGVILDEYEMKFEK--SEGIASTVYTSOMNSVOL 510  
QY 480 TGLKAGLIYVOVARVAVAGYGRYSGKMYFQMTF--AEYTSIOEKPLITIGSSAGLVF 538  
DB 511 DGLRPDARIYVOVARVAVAGYGRYSGKMYFQMTF--AEYTSIOEKPLITIGSSAGLVF 570  
QY 539 LIAVVYIAI 547  
DB 571 VVAVVYIAI 579

```

RESULT 15
PCT-US01-03800A-2273
: Sequence 2273, Application PC/TUS0103800A
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: APPLICANT: Tang, Y, Tom et al
: TITLE OR INVENTION: Novel Nucleic Acids and Polypeptides
: FILE REFERENCE: 21272-030
: CURRENT APPLICATION NUMBER: PCT/US01/03800A
: CURRENT FILING DATE: 2001-02-05
: PRIOR APPLICATION NUMBER: 09/566,875
: PRIOR FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: 09/496,914
: PRIOR FILING DATE: 2000-02-03
: NUMBER OF SEQ ID NOS: 2700
: SOFTWARE: Custom
: SEQ ID NO 2273
: LENGTH: 1007
: TYPE: 'PRT'
: ORGANISM: Homo sapiens
PCT-US01-03800A-2273

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Query Match	62.2%:	Score 1800.5:	DB 1:	Length 1007:
Best Local Similarity	61.9%:	Pred. No. 1e-158:		
Matches 340:	Conservative	79:	Mismatches 119:	Indels 11:
				Gaps
4	AVETLTMDSTTAAETAEAGMMVHPSPGMEVEVSGYDENMNTIRTYQVCNVEFESSQNNMLTKF	63		
Db	46 ALBETLTMDTQWVYSELAMTSHPESGMEVEVSGYDEAMNPTRTYQVCNVEFESSQNNMLTKF	105		
QY	64 IRRGAHRHIVEKESVYRCSSIPYPSGCKTFYLYXYEADPEFSATKTPNNMENFWK	123		
Db	106 IMRWDVQRYVVELKTFVRCNCSIPTNPISGCKTFELFYFEADSDVASASPFWMENFYK	165		
QY	124 VDTIAADESFQYDVLGGRVMKINTVEYRSRGPYRSRGFYLAFODYGGCMLIAVRFYRKC	183		
Db	166 VDTIAPEESRILDAG----RVNVTKYRSRGPISLKAIFYLAFODGACMSLISVAFYKCC	221		
QY	184 PRITONGAIFQETLSGAESTSLVANGSCLINAAEYDVPRIKLYCNGJSEMIYVIGRCMK	243		
Db	222 ASTAGCALPTELITGAEPYSLVIAGTCTIPANVEVSPPLKYCNGDEEMVPIGACTCA	281		
QY	244 AGFAVAVENGTVCGCGSPGTFKANQGDCACTHCPINSRTTSEGATNCVCRNGYRADIDL	303		
Db	282 TGHEPPAKESQCRPCPGSYKAKQAGGPPOLPCPPNSRTTSPASISICTCHNNFYRADSDSA	341		
QY	304 DMPCTTIPSAFOAVISSVNETSLMLEMTPPRDSGREDLVYIITKSC--GSGRGACRC	361		
Db	342 DSACTVPSPRGIVSNVNETSLILEMSEPRDYGVDLLYVITCKKHGAGGASACSRC	401		
QY	362 GDNQVQAPRQGLDEPRITISDLLAHQYFEELOVANGTQDPSPEPQFASVINITTNOA	421		
Db	402 DDNVEFVPRQGLSEPRVHTSHLAHRTYFEQVANGVSGSPLPRKAAVNITTNOA	461		
QY	422 PSAVIMHQVSRVDSITLSNSQPDQPNVILYDELQYKEKELSEYNATAKSPNTV--	479		
Db	462 PSEVYTLALHSSSSSLTISMAPERPBNGLIYEMKYEK--SEGIASTVYSQNNNSVL	519		
QY	480 TGLKAGAIYFOVBARIVAGYGRISGAMTYQYTFE-ABEQTSLQELPLIIGSSAAGLVF	538		
Db	520 DGLRPDARYVQVBARIVAGYQYSRPAEFETTSERGSQAQLOEQPLIVGSATAGLVF	579		
QY	539 LIAYVYVIT 547			
Db	580 VYAVVYVIT 588			

Search completed: February 1, 2002, 09:59:47  
Job time: 407 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 1, 2002, 10:00:07 ; Search time 26.14 Seconds  
(without alignments)  
874.598 Million cell updates/sec

Title: US-09-378-759-11\_COPY\_1\_547  
Perfect score: 2895  
Sequence: 1 LAAVEETLMDSTATAELG.....IISSAAGVFLAAVVVIAL 547

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 202503 seqs, 41795235 residues

Total number of hits satisfying chosen parameters: 202503

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New: \*  
1: /cgn2\_6/ptodata/1/paa/PCN\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2083.5	72.0	984	US-60-341-631-3
2	1485.5	51.3	1037	US-60-339-995-3
3	1414	48.8	942	US-10-004-542-2
4	1410	48.7	1036	US-09-971-708-2
5	1410	48.7	1130	US-09-922-138-2
6	1395	48.2	1035	US-09-871-708-3
7	784.5	27.1	265	PCN-US01-30539-4
8	783.5	27.1	265	PCN-US01-30539-5
9	783.5	27.1	265	PCN-US01-30539-6
10	686	23.4	295	PCN-US01-30539-2
11	678	23.4	178	US-09-922-138-10
12	666.5	23.0	180	US-09-922-138-12
13	531.5	18.4	260	US-09-922-138-11
14	429.5	14.8	127	US-09-922-138-13
15	405	14.0	116	US-10-029-386-33374
16	341.5	11.8	119	US-10-029-386-32097
17	200	6.9	59	US-09-922-138-15
18	174.5	6.0	1518	US-09-976-594-531
19	174	6.0	1461	US-09-976-594-531
20	158.5	5.3	5701	US-10-029-386-32438
21	153	5.3	760	US-09-611-526-3462
22	149	5.1	1382	US-09-971-873-7
23	148	5.1	1351	US-09-970-318-4
24	146.5	5.1	1948	US-09-800-198-45
25	144	5.0	595	US-10-029-386-32978
26	143.5	5.0	980	US-09-908-193-22

27	140.5	4.9	588	US-10-029-386-33963	Sequence 33963, A
28	140	4.8	1502	US-09-800-198-44	Sequence 44, Appl
29	136.5	4.7	1252	US-09-908-193-21	Sequence 21, Appl
30	135.5	4.7	48	US-10-029-386-32098	Sequence 32098, A
31	135	4.7	1247	US-09-908-193-2	Sequence 2, Appl
32	134.5	4.6	1252	US-09-908-193-19	Sequence 19, Appl
33	134.5	4.6	1253	US-09-908-193-20	Sequence 20, Appl
34	131	4.5	1008	US-09-908-193-11	Sequence 11, Appl
35	126	4.4	886	US-09-923-559-11	Sequence 57, Appl
36	125.5	4.3	2012	US-09-922-647-11	Sequence 5, Appl
37	120	4.1	488	US-09-800-198-57	Sequence 55, Appl
38	119.5	4.1	1375	US-09-950-149-5	Sequence 27, Appl
39	118	4.1	1260	US-09-800-198-55	Sequence 2857, Ap
40	117.5	4.1	570	US-10-024-918-27	Sequence 101, App
41	116	4.0	1138	US-10-021-660-101	Sequence 113, App
42	116	4.0	1786	US-09-873-676-113	Sequence 61, Appl
43	115.5	4.0	2167	US-09-778-927A-61	Sequence 2, Appl
44	115	4.0	1107	US-09-977-053-2	Sequence 56, Appl
45	115	4.0	1395	US-09-800-198-56	

## ALIGNMENTS

RESULT 1  
US-60-341-631-3  
Sequence 3, Application US/60341631  
GENERAL INFORMATION:  
APPLICANT: Spallmann, Frank  
TITLE OF INVENTION: Silos-Santiago, Immaculada  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
FILE REFERENCE: MP12001-233PI(M)  
CURRENT APPLICATION NUMBER: US/60/341.631  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 984  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-60-341-631-3

Query Match	Best Local Similarity	72.0%	Score 2083.5;	DB 7;	Length 984;
Matches 374;	Conservative	87;	Pred. No. 1.8e-170;	Mismatches 84;	Indels 3;
				Gaps 2;	
QY	2	LAAVEETLMDSTATAELGMMVHPPSGMEVSGYDENMTTFTYQVNCNVRESSONMRLRT	61		
DB	15	VAAWETLMDRTATLAEGLWTANPASGHEVSGYDENMTTFTYQVNCNVRESSONMRLRT	74		
QY	62	KPIRRGARRHVEKRSVRCSSIPVPSCKETFMILYYEADFDSATTFPPMMENPM	121		
DB	75	TFINRGARRHRYTMRRTVRDCSSLPVPSCKETFMILYYEADFDSATTFPPMMENPM	134		
QY	122	VKVDITADESFOVDAGGRVMTKTEVRSGPVSRCGFYLAODVGGCSLAAYRFR	181		
DB	135	LKVDTIADESFSGYVDGGRVMTKTEVRSGPVSRCGFYLAODVGGCSLAAYRFR	194		
QY	182	KCPRIIONGALFOETLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGRM	241		
DB	195	KCPRIIONGALFOETLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEMLVPIGRM	254		
QY	242	CKAGFEVENGTCVRCGPGSTFRKANGDEACTHCPINSRTSGATNCVCRNGYTRADID	301		
DB	255	CKGVEP-ENSVACKACFACFASQABEGSCHSPNSPAPASPCICRGTGYRADPD	313		
QY	302	PLMDPCTTISAPQAVISSVNETSLMEWTTPRDSGGRBDLYVNIICKSGSGRACTRC	361		
DB	314	PPEVACTSVPSGPRNVISIVNETSILEWHPPRETGGRDVTYNIICKSGGRACTRC	373		
QY	362	GDNVQYARQLGLTEPRITISDLAHTQYTFELQAVNGVTDSPSPQFASVNTTNOAA	421		

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Db 374 DDNEVEPRQGLTECKRSISLSLAHPTPTDIOANGVSSKSPFPQHVSVNTTNOAA 433
OY 422 PSASIMHQSRTVDSITLMSOPDQPNGLVDELOYEKEKELSEYNATAIKSTNT--V 479
Db 434 PSTVIMHQSRTVDSITLMSOPDQPNGLVDELOYEKEKELSEYNATAIKSTNTARI 493
OY 480 TGLKGAIVYQVARKATVAGRGYSKMYFOTMTEAEYQTSIOEKPLIIGSSAAGLVFL 539
Db 494 DGLRGMYVVOVARKATVAGRGYSKMYFOTLDDDKSELRLPLIAGSAAAGVYFV 553
OY 540 IAVVIAI 547
Db 554 VSLVAISI 561

RESULT 2
US-60-339-995-3
; Sequence 3, Application US/60339995
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Mijoung
; TITLE OF INVENTION: Methods and Compositions to Treat
; TITLE OF INVENTION: Cardiovascular Disease Using 1419, 58765 and 2210
; FILE REFERENCE: MP12001-291P1(M)
; CURRENT APPLICATION NUMBER: US/60/339,995
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1037
; TYPE: PR1
; ORGANISM: Homo Sapien
US-60-339-995-3

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Query Match 51.3%; Score 1485.5; DB 7; Length 1037;
Best Local Similarity 50.7%; Pred. No. 4.3e-119; Indels 11; Gaps 7;
Matches 276; Conservative 107; Mismatches 150;

OY 6 EETLMDSTTAAELGMMVHPSPGMEVSGYDENMNTIRTYOVCVFESSONMNLRTKFR 65
Db 60 EVNLIDRTVAGDGLWIAFPKNGMEIGEVDEYAPRHTYQVCKVMEONONMNLTSWIS 119
OY 66 RGAHRIHVEKESVRCDSIPVSGCKETFNLYYEADPDSATKTFPMMEPNWYKVD 125
Db 120 NEGASRIETIELKTRLCNLSLPGLGCKETFNMYFESDDNGR---NIKENQIKID 175
OY 126 TIADESFOVDLGRVWKINTEVRSFGPVRSRGFYLAFOYGGMSLIAVRYFKCPR 185
Db 176 TIADESFTEDLDGRVWKINTEVRSFGPVRSRGFYLAFOYGGMSLIAVRYFKCPS 235
OY 186 IIONGAIFOETLSGAESTSLVAARSCIANAEVDVPIKLYCNDGEMVLVPIGCMKAG 245
Db 236 VYRHLAVPRDITGADSQLLEVSGCV-NHSVYDEPKMCSAEGEWLVPIGCMKAG 294
OY 246 PEAVANGVCCPGSTGKANOGEACHTCPINSRTTSGATNCYCRNGYRARDLPDM 305
Db 295 YEE-KNGT-CQVCRPGFRAKSHPHIOSCKCPRHSTTHEATSCCEXDYRRSDPPTM 352
OY 306 PCTTIPSAQAVISSVNETSLMLEWTPPRDSGREDLVYNIICSGSGRACIRGCINV 365
Db 353 ACTRPPSAPRNAMISWNETSVFLEWIPRADTGGRKDVSYIACKCNCSHAGVCEEGGHV 412
OY 366 QYAPROLGTERIRIYISDLAHTOYTFEIOAVNGVTDOSPSPASVNTTNOAAPSAY 425
Db 413 RYLPKROSGKNTSVMWVDLAFNTFTFEIAYNGVSDLSFGAKOYVSVNVTNNOAAPSAY 472
OY 426 SIMHOVSRTVDSITLMSOPDQPNGLVDELOYEKEKELSEYNATAIKSPINTVT--GLK 483
Db 473 TAVKAKIKAKNSISLMSOPDQPNGLVDELOYEKEKELSEYNATAIKSPINTVT--GLK 531
OY 484 AGAIYVOVARTVAGRGYSKMYFOTMTEAEYQTSIOEKPLIIGSSAAGLVFLAVY 543

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Db 532 PASVYFQIRARTVAGRGYSKMYFOTMTEAEYQTSIOEKPLIIGSSAAGLVFLAVY 590
OY 544 VIAI 547
Db 591 GVLL 594

RESULT 3
US-10-004-542-2
; Sequence 2, Application US/10004542
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomichy, Boris
; APPLICANT: Gerhardt, Brenda
; APPLICANT: Walke, D. Wade
; APPLICANT: Fiddie, Carl Johan
; TITLE OF INVENTION: Novel Human Kinase and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0260-USA
; CURRENT APPLICATION NUMBER: US/10/004,542
; PRIOR FILING DATE: 2001-10-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 942
; TYPE: PR1
; ORGANISM: homo sapiens
US-10-004-542-2

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Query Match 48.8%; Score 1414; DB 6; Length 942;
Best Local Similarity 48.1%; Pred. No. 5.2e-113; Indels 12; Gaps 7;
Matches 260; Conservative 106; Mismatches 162;

OY 9 LMDSTTAAELGMMVHPSPGMEVSGYDENMNTIRTYOVCVFESSONMNLRTKFR 68
Db 131 LMDSTTAAELGMMVHPSPGMEVSGYDENMNTIRTYOVCVFESSONMNLRTKFR 190
OY 69 AHRHVEKESVRCDSIPVSGCKETFNLYYEADPDSATKTFPMMEPNWYKVD 128
Db 191 AHRHVEKESVRCDSIPVSGCKETFNLYYEADPDSATKTFPMMEPNWYKVD 246
OY 129 ADESFQVDLGRVWKINTEVRSFGPVRSRGFYLAFOYGGMSLIAVRYFKCPR 188
Db 247 ADESFQVDLGRVWKINTEVRSFGPVRSRGFYLAFOYGGMSLIAVRYFKCPR 306
OY 189 NGAIPOETLSGAESTSLVAARSCIANAEVDVPIKLYCNDGEMVLVPIGCMKAG 248
Db 307 NLAEPDITPRDSSSLVARSQVSAERDLP-KLYCGADGDMVLVPIGCMKAG 365
OY 249 VENGTVRCGPGSTGKANOGEACHTCPINSRTTSGATNCYCRNGYRARDLPDM 308
Db 366 IEGS--CHACRPFGYKAFAGNTKSCKCPHSLYMEATSVCCCEGYFAEADPDSMACT 423
OY 309 TITSAPQAVISSVNETSLMLEWTPPRDSGREDLVYNIICSGSGRACIRGCINV 368
Db 424 RPPSAPRNAMISWNETSVFLEWIPRADTGGRKDVSYIACKCNCSHAGVCEEGGHV 483
OY 369 PROGLTERIRIYISDLAHTOYTFEIOAVNGVTDOSPSPASVNTTNOAAPSAY 427
Db 484 PRHGLNNSVYIYLDVDFSVNVTFTFEIAYNGVSDLSFGAKOYVSVNVTNNOAAPSAY 542
OY 428 MHOVSRTVDSITLMSOPDQPNGLVDELOYEKEKELSEYNATAIKSPINTVT--GLK 485
Db 543 VRKMAQONSIALSWQPARSNGALIDYEYKEKELSEYNATAIKSPINTVT--GLK 602
OY 486 AIYVOVARTVAGRGYSKMYFOTMTEAEYQTSIOEKPLIIGSSAAGLVFLAVY 545
Db 603 TKYFHRIRVARTVAGRGYSKMYFOTMTEAEYQTSIOEKPLIIGSSAAGLVFLAVY 661

```







SEQ ID NO 6  
LENGTH: 265  
TYPE: PRT  
ORGANISM: Mus musculus  
PCT-US01-30539-6

Query Match 27.1%; Score 783.5; DB 1; Length 265;  
Best Local Similarity 56.3%; Pred. No. 1.3e-59;  
Matches 143; Conservative 49; Mismatches 55; Indels 7; Gaps 3;

QY 3 AAVETLMDSTATAELGMMVHPSPSGMEVSGYDENMTIRTYOVCNVPESSONMLRTK 62  
DB 17 AAKVILLDSKAQOETLEWISSPPSGMEISGLDENTPIRTYOVCOVMEPNQNMMLRTN 76  
QY 63 FRRGARRHIVEMKFSVRDCSSIPSVGSCKETENLYYEADSDSKTFPPNMENPMV 122  
DB 77 WISGNMGRFVELKFTLRDCNLSIPGLVLTCKETFNLYETDID---TGRNIREMLKY 132  
QY 123 KVDITADESFQVDLGRVWKINTEVRSFGVSRSGFYLAFOVGGCMLIAVRFYRK 182  
DB 133 KIDITADESFQVDLGRVWKINTEVRSFGVSRSGFYLAFOVGGCMLIAVRFYRK 192  
QY 183 CPTIONGALFOETLSAESTSLVAAGSCLANA-EVDVPIKLYCGDDEMLVPIGRMC 241  
DB 193 CMTIVENLAVFPDVTGSEFSLVEVGTCSVAEEAENSPPRMHCSAEDEMLVPIGRMC 252  
QY 242 CKAGFEAVENGTVG 255  
DB 253 CKAGYQ--QKGDTC 264

RESULT 10  
PCT-US01-30539-2  
Sequence 2, Application PC/TUS0130539  
GENERAL INFORMATION:  
APPLICANT: PE CORPORATION (NY)  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
FILE REFERENCE: CL001156PCT  
CURRENT APPLICATION NUMBER: PCT/US01/30539  
CURRENT FILING DATE: 2001-03-06  
PRIOR FILING DATE: 09/79, 345  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 295  
TYPE: PRT  
ORGANISM: Human  
PCT-US01-30539-2

Query Match 23.7%; Score 686; DB 1; Length 295;  
Best Local Similarity 51.4%; Pred. No. 3.5e-51;  
Matches 131; Conservative 46; Mismatches 74; Indels 4; Gaps 3;

QY 4 AVEETLMDSTATAELGMMVHPSPSGMEVSGYDENMTIRTYOVCNVPESSONMLRTK 63  
DB 33 AEEVILLDSKAQOETLEWISSPPSGMEISGLDENTPIRTYOVCOVMEPNQNMMLRTN 92  
QY 64 IRRGARRHIVEMKFSVRDCSSIPSVGSCKETENLYYEADSDSKTFPPNMENPMV 123  
DB 93 ISRGRRGRFVELKFTLRDCNLSIPGLVLTCKETFNLYETDID---TGRNIREMLKY 151  
QY 124 VDTIADESFQVDLGRVWKINTEVRSFGVSRSGFYLAFOVGGCMLIAVRFYRK 183  
DB 152 IDTIADESFQVDLGRVWKINTEVRSFGVSRSGFYLAFOVGGCMLIAVRFYRK 211  
QY 184 PRTIONGALFOETLSAESTSLVAAGSCLANA-EVDVPIKLYCGDDEMLVPIGRMC 242  
DB 212 RATVKGALFPAATASAFSTLVEAGTCVAHSEGEPSPPRMHCSAEDEMLVPIGRMC 271

QY 243 KAGFEAVENGTVG 257  
DB 272 SAGFO--ERGDICG 284

RESULT 11  
US-09-922-138-10  
Sequence 10, Application US/09922138  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Meyers, Rachel  
TITLE OF INVENTION: KINASES AND USES THEREFOR  
FILE REFERENCE: 38155-20030.00  
CURRENT APPLICATION NUMBER: US/09/922,138  
CURRENT FILING DATE: 2001-11-28  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 178  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Consensus amino acid sequence  
US-09-922-138-10

Query Match 23.4%; Score 678; DB 5; Length 178;  
Best Local Similarity 68.7%; Pred. No. 8.6e-51;  
Matches 123; Conservative 26; Mismatches 28; Indels 2; Gaps 2;

QY 6 EETLMDSTATAELGMMVHP-PSGMEVSGYDENMTIRTYOVCNVPESSONMLRTK 64  
DB 1 EYLLDTKATGELGMLTYVPVSGMEVSGLDENNRPIRTYOVCNVPEPNQNMMLRTN 60  
QY 65 RRGARRHIVEMKFSVRDCSSIPSVGSCKETENLYYEADSDSKTFPPNMENPMV 124  
DB 61 ERGARRHIVEMKFSVRDCSSIPSVGSCKETENLYYEADSDSKTFPPNMENPMV 124  
QY 125 DTTIADESFQVDLGRVWKINTEVRSFGVSRSGFYLAFOVGGCMLIAVRFYRK 183  
DB 120 DTTIADESFQVDLGRVWKINTEVRSFGVSRSGFYLAFOVGGCMLIAVRFYRK 178

RESULT 12  
US-09-922-138-12  
Sequence 12, Application US/09922138  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Meyers, Rachel  
TITLE OF INVENTION: KINASES AND USES THEREFOR  
FILE REFERENCE: 38155-20030.00  
CURRENT APPLICATION NUMBER: US/09/922,138  
CURRENT FILING DATE: 2001-11-28  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Consensus amino acid sequence  
US-09-922-138-12





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 1, 2002, 09:54:55 ; Search time 26.14 Seconds  
(without alignments)  
1550.933 Million cell updates/sec

Title: US-09-378-759-11

Perfect score: 5116

Sequence: 1 LLAARETLMDSMTATAELG.....ILNSTQVMAQNMQISVEV 970

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 202503 seqs, 41795235 residues

Total number of hits satisfying chosen parameters: 202503

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pap.\*
- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3899.5	76.2	984	7 US-60-341-631-3	Sequence 3, Appl
2	3014	58.9	1037	7 US-60-339-995-3	Sequence 3, Appl
3	2837	55.5	1036	5 US-09-971-708-2	Sequence 2, Appl
4	2837	55.5	1035	5 US-09-922-138-2	Sequence 2, Appl
5	2811	54.9	1035	5 US-09-971-708-3	Sequence 3, Appl
6	2161.5	42.2	942	6 US-10-004-542-2	Sequence 2, Appl
7	1793	35.0	406	5 US-09-760-446A-1452	Sequence 1452, Ap
8	1150	22.5	270	5 US-09-760-446A-1496	Sequence 1496, Ap
9	1103.5	21.6	277	5 US-09-760-446A-1538	Sequence 1538, Ap
10	822	16.1	189	5 US-09-760-446A-2141	Sequence 2141, Ap
11	784.5	15.3	265	1 PCT-US01-30539-4	Sequence 4, Appl
12	783.5	15.3	265	1 PCT-US01-30539-5	Sequence 5, Appl
13	783.5	15.3	265	1 PCT-US01-30539-6	Sequence 6, Appl
14	771	15.1	308	6 US-10-004-542-4	Sequence 4, Appl
15	771	15.1	334	5 US-09-971-708-5	Sequence 5, Appl
16	686	13.4	295	1 PCT-US01-30539-2	Sequence 2, Appl
17	684	13.4	190	5 US-09-760-446A-1492	Sequence 1492, Ap
18	678	13.3	178	5 US-09-922-138-10	Sequence 10, Appl
19	672	13.1	222	5 US-09-760-446A-2225	Sequence 2225, Ap
20	670	13.1	204	5 US-09-760-446A-2137	Sequence 2137, Ap
21	666.5	13.0	180	5 US-09-922-138-12	Sequence 12, Appl
22	639.5	12.5	206	5 US-09-760-446A-1652	Sequence 1652, Ap
23	597	11.7	1382	5 US-09-971-873-7	Sequence 7, Appl
24	595	11.6	351	5 US-09-760-446A-1339	Sequence 1339, Ap
25	595	11.6	541	5 US-09-864-291-20	Sequence 20, Appl
26	594	11.6	509	5 US-09-971-873-8	Sequence 8, Appl

27	591	11.6	376	5 US-09-760-446A-2013	Sequence 2013, Ap
28	586	11.5	256	5 US-09-967-854-4	Sequence 4, Appl
29	586	11.5	256	5 US-09-840-704-4	Sequence 4, Appl
30	576.5	11.3	1138	6 US-10-021-660-101	Sequence 101, Appl
31	574	11.2	271	5 US-09-971-873-41	Sequence 41, Appl
32	562.5	11.0	1256	5 US-09-632-507A-2	Sequence 2, Appl
33	554	10.8	280	6 US-10-003-690-8	Sequence 8, Appl
34	551	10.8	823	5 US-09-886-319A-63	Sequence 63, Appl
35	549.5	10.7	1256	5 US-09-632-507A-14	Sequence 14, Appl
36	547	10.7	822	5 US-09-886-319A-64	Sequence 64, Appl
37	539.5	10.5	1256	5 US-10-021-660-112	Sequence 112, Appl
38	539	10.5	1255	5 US-09-806-703A-4	Sequence 4, Appl
39	538.5	10.5	937	5 US-09-974-298-129	Sequence 129, Appl
40	538	10.5	1255	5 US-09-632-507A-1	Sequence 1, Appl
41	537	10.5	619	5 US-09-971-873-9	Sequence 9, Appl
42	531.5	10.4	260	6 US-10-029-386-33374	Sequence 33374, A
43	530	10.4	885	1 PCT-US01-24104A-52	Sequence 52, Appl
44	522	10.2	822	5 US-09-966-147-2	Sequence 2, Appl
45	520.5	10.2	1210	5 US-09-725-433-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-60-341-631-3  
; Sequence 3, Application US/60341631  
; GENERAL INFORMATION:  
; APPLICANT: Spaltmann, Frank  
; APPLICANT: Silos-Santiago, Immaculada  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1421 AND 14381  
; FILE REFERENCE: MPI2001-293P1(M)  
; CURRENT APPLICATION NUMBER: US/60/341,631  
; CURRENT FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 984  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-60-341-631-3

Query Match	76.2%	Score 3899.5;	DB 7;	Length 984;
Best Local Similarity	73.8%;	Pred. No. 3.4e-274;		
Matches 712;	Conservative 130;	Mismatches 120;	Indels 3;	Gaps 2;
QY	2	LAARETLMDSMTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCNVFPSSQNMLRT	61	
Db	15	VAAAEETLMDTRTATAELGWTANPASPGEVSGYDENLNTIRTYQVCNVFPNQNNMLLT	74	
QY	62	KPIRRGAHRIHVEMKFSVRDCSSIPSPGSKETFNLYYEAADFSDATKTFPNMNPW	121	
Db	75	TFINRGAHRIYTEMRTVTRDCSSLPNPVPGSKETFNLYYETDSVIATKSAFSEAPY	134	
QY	122	VKVDITAADESFSQVLDGGRVKNKINTEVRSGPVSRSGFYLAFOQDYGCMSLIAVRVYR	181	
Db	135	LKVDITAADESFSQVDFGGRLMKVNTVRSFGPLTRNGFYLAFOQDYGCMSLLSVRVFEK	194	
QY	182	KCPRIQNGALFOETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPVIGRCM	241	
Db	195	KCPISVQNFVFPETMTGAESTSLVTARGCTIPNAEEVDVPIKLYCNGDGEWVPIGRCT	254	
QY	242	CKAGFEAVENTVCGPCSPCTFKANQGDCACTHCPINSTRTTSEGAATNCVCRNGYRADLD	301	
Db	255	CKPGYEP-ENSVACKACPACTFKASQAECSCHPSNSRSPAEASPICTCTGYRADFD	313	
QY	302	PLDMPCTISAPQAVISSVNETSLMLEWTPPRDSGGREDLVNITCKSCSGRGATRC	361	
Db	314	PPEVACTSVSPGPRNVISVNETSIILEWHPHRETGTGRDDVTYNIICKRADRRSCRC	373	
QY	362	GDNVQYAPRQGLTEPRIYISDLLAHTQYTFEIQAVNGVTDQSPSPQFASVNTITNOAA	421	

Db 374 DDNVEFPRQLGTECRVSISLWAHPYTFDIOANGVSSKSPFFPHQHVSNITNQAA 433  
Qy 422 PSAYSIMHOVSRTVDSITLWSQDPQNGVILDEYLOQYKEKELSEYNATAIKSPNT -V 479  
Db 434 PSTPIHQVSATWRSITLWSQDPQNGVILDEYLOQYKEKELSEYNATAIKSPNTARI 493  
Qy 480 TGLKAGAIYFQVRRARTVAGRYSGRMVYQTMTEAEYQYISQKPLLIYSSAAGLVFL 539  
Db 494 DGLRPGMVVYVVRARTVAGRYSGRMVYQTMTEAEYQYISQKPLLIYSSAAGLVFL 553  
Qy 540 IAVVIAIVCNRRGERADSEYTKLOHYTSGHITPGMKIYIDPTEYEDNEAVREFAKE 599  
Db 554 VSLVAISVCRKRAYSKAEAVYSKLOHYTSGRSGPMKIYIDPTEYEDNEAVREFAKE 613  
Qy 600 IDISCVKIEQVIGAGEFGEVSGHKLPGKREIFVAIKTKAGYSEKQRDFLEASIMG 659  
Db 614 IDVSFVKIEVIGAGEFGEVSGHKLPGKREIFVAIKTKAGYSEKQRDFLEASIMG 673  
Qy 660 QPDHNPVHLEGVVTKSTPVMIIITFEFMENGSLDSFLRQNDGQFTVIOLVGMRLGIAAGMK 719  
Db 674 QPDHNPVHLEGVVTKSTPVMIIITFEFMENGSLDSFLRQNDGQFTVIOLVGMRLGIAAGMK 733  
Qy 720 YLADNNYVHRDLAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTVTSAL3GKFPRTAP 779  
Db 734 YLADNNYVHRDLAARNILVNSNLVCKVSDFGLSRPLEDDTSDPTVTSAL3GKFPRTAP 793  
Qy 780 EAIQYRKFTSASDVMSYGIIVMEVMSYGERPYWDMTNDVINAIBQYRLPPMDCPAL 839  
Db 794 EAIQYRKFTSASDVMSYGIIVMEVMSYGERPYWDMTNDVINAIBQYRLPPMDCPAL 853  
Qy 840 HOLMDCWQKDRNHRPKGQIVNTLDKMRNPNSLKAMAPLSSGKINLPLDRTIPDYTSF 899  
Db 854 HOLMDCWQKDRNHRPKGQIVNTLDKMRNPNSLKAMAPLSSGKINLPLDRTIPDYTSF 913  
Qy 900 NTVDLEIAIKMGOYKESFANAGFTSFVVSOMMEDILRVGVTLAGHOKKILNSIQVMR 959  
Db 914 TVVDDWLSAIAKVVQYRDSFLTAGFTSLQVLTQMTSEDLIRIGITLAGHOKKILNSIHSR 973  
Qy 960 AQNQ 964  
Db 974 VQISQ 978

RESULT 2  
US-60-339-995-3  
; Sequence 3, Application US/60339995  
; GENERAL INFORMATION:  
; APPLICANT: Logan, Thomas Joseph  
; APPLICANT: Chun, Miyoung  
; TITLE OF INVENTION: Methods and Compositions to Treat  
; TITLE OF INVENTION: Cardiovascular Disease Using 1419, 58765 and 2210  
; FILE REFERENCE: MPI2001-291P1(M)  
; CURRENT APPLICATION NUMBER: US/60/339,995  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1037  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-60-339-995-3

Query Match 58.9%; Score 3014; DB 7; Length 1037;  
Best Local Similarity 57.8%; Pred. No. 5.2e-210;  
Matches 568; Conservative 163; Mismatches 215; Indels 36; Gaps 12;  
Qy 6 BETLMDSTTAAELAGWVHPSPGWEVSGYDENNTIRTVQCNVFNSSONMLRKFIR 65  
Db 60 EVNLDSTRTVMGLGWTAFAPKNGWEEIGEDENYAPIHTYQVCKVMEQONQNLWLSWIS 119  
Qy 66 RGAHRHIVEMKFSVRDCSSIPSPGSKETFNLYYYEADFDSATKTFPNWMPNVPVKVD 125

Db 120 NEGASRIFTELFTLRDCNSLPGGLGCTKETFMNYFFSDQNGR ----NKENOYIKID 175  
Qy 126 TTAADSEFSQVDLGRVVKINTEVRSFGYSLAFODYGGCMSLIAVRFYRKCPR 185  
Db 176 TTAADSEFTFELDGRVVKINTEVRSFGYSLAFODYGGCMSLIAVRFYRKCPR 235  
Qy 186 ITONGAIFQETLSGABESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRCMKAG 245  
Db 236 VYHRLAVFDTITGADSSQLLEVSGSCV -NHSVTDEPPKMHCSABGEWLVPIGRCMKAG 294  
Qy 246 FEAVENGTVCRGCPSTGFRKANQDEACTHCPINRSRTSEGATNCVCRNGYYRADLDPLDM 305  
Db 295 YEE-KNGT-CQVCRPGFFKASPHIQSCGKCPHSHYTHEEASTSCVCEKDYFRRESDPPTM 352  
Qy 306 PCTTIPSAQVATISSVNETSLMEWTPPRDSSGREDLVNIICKSGSGRGACTRGDNV 365  
Db 353 ACTRPPSAPRNALSNVNETSVFLEWIPPADTGGKDVSYIACKKNSHAGVCECGGHV 412  
Qy 366 QYAPRQLGLTEPRIYISDLAHTQYTFEIOAVNGVTDQSPFPOFASVNTTNOAAPSAV 425  
Db 413 RYLPQSGGLKNTSMVMYDLLAHTNYTFEAVNGVSDLSFGARQYVSVNVTINQAAPSPV 472  
Qy 426 SIMHOVSRTVDSITLWSQDPQNGVILDEYLOQYKEKELSEYNATAIKSPNTVT --GLK 483  
Db 473 TNYKKGKIAKNSLSMQEPRNGIILEYKIFKFKD-QETSYTIKSKETITAEGLK 531  
Qy 484 AGAIYFQVRRARTVAGRYSGRMVYQTMTEAEYQYISQKPLLIIGSSAAGLVFLAVV 543  
Db 532 PASVYVQIRARTAAAGYGVFSRRFEPET-TPVFAASDQSQIPVIAVSVTVGVILLAVI 590  
Qy 544 VIAIV-----CNRR-----GFERADSEYTKLOHYTSGHI-TPGMKIY 580  
Db 591 GVLLSGSCCECGGRASSLCAVAHPILINWCGRYSKAKQDPEEKMHFNHGHILPGVRY 650  
Qy 581 IDPTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVSGHKLPGKREIFVAIKTKL 640  
Db 651 IDPTYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVSGHKLPGKREIFVAIKTKL 710  
Qy 641 SGYTEKORRRDPLSEASIMGQDPHNPVHLEGVVTKSTPVMIIITFEFMENGSLDSFLRNDG 700  
Db 711 VGYTEKORRRDPLSEASIMGQDPHNPVHLEGVVTKSTPVMIIITFEFMENGSLDSFLRNDG 770  
Qy 701 QFTVQLVGLMRLGIAAGMKYLDAMNIVHRDLAARNILVNSNLVCKVSDFGLSRPLEDDTS 760  
Db 771 QFTVQLVGLMRLGIAAGMKYLDAMNIVHRDLAARNILVNSNLVCKVSDFGLSRPLEDDTS 829  
Qy 761 DPTYTSALGGKPEIRWTAPAEAIQYRKFTSASDVMSYGIIVMEVMSYGERPYWDMTNDV 820  
Db 830 EAAVTR-GGKIPIRWTAPAEAIQYRKFTSASDVMSYGIIVMEVMSYGERPYWDMTNDV 888  
Qy 821 NAIQDYRLPPMDCPALHOLMDCWQKDRNHRPKGQIVNTLDKMRNPNSLKAMAPL 880  
Db 889 KAVEGYRLPPMDCPALHOLMDCWQKDRNHRPKGQIVNTLDKMRNPNSLKAMAPL 948  
Qy 881 SSGINLPLDRTIPDYTSFNTVDLEIAIKMGOYKESFANAGFTSFVVSOMMEDILRV 940  
Db 949 SCRVSNLLAEHSPGSGAVRSVGEWLEIAIKMGRYTEIFMENGYSMDAVAQVTLDELRL 1008  
Qy 941 GVTLAGHOKKILNSIQVMRAQM 962  
Db 1009 GVTLAGHOKKILNSIQVMRAQM 1030

RESULT 3  
US-09-971-708-2  
; Sequence 2, Application US/09971708  
; GENERAL INFORMATION:  
; APPLICANT: Origene Technologies, Inc  
; TITLE OF INVENTION: Human EphA6 Gene and Polypeptide  
; FILE REFERENCE: OGT 160 102 R1  
; CURRENT APPLICATION NUMBER: US/09/971,708  
; CURRENT FILING DATE: 2001-10-09



NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 2  
LENGTH: 1036  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-971-708-2

Query Match 55.5%; Score 2837; DB 5; Length 1036;  
Best Local Similarity 53.6%; Pred. No. 3.4e-197;  
Matches 539; Conservative 167; Mismatches 240; Indels 60; Gaps 13;

QY 9 LMDSTTATLGMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKFIERRG 68  
Db 37 LDDTTVLGELGWKTYPLNGWDAITEMDEHNRPITHYQVCNVMEPNQNNWLRTNWSRDA 96

QY 69 ARIHVEKFSVRDCSSIPSPVPGSKETFNLYYEADPDSATKTFPNMNPWKVDTIA 128  
Db 97 AOKIYVEMKFTLRDCNSIPWLGTKETFNLFYMESDESHGKFKP-----NOYTKIDTIA 152

QY 129 ADESFQVDLGRVNMKINTEVRSGFVRSRSGFYLAFOYDYGCMSLIAVRVYRKCPRIIQ 188  
Db 153 ADESFQMDLGRILKLTREVGPIERKGFYLAFOYDYGCMSLIAVRVYRKCPRIIQ 212

QY 189 NGAIFQETLSGAESTSLVAARGSCIANAEVDVPILKYCNGDGEWLPVIGRCMCKAGFEA 248  
Db 213 NLAMFPDPIPRVDSLSLVEVRGSCVKAERDTP-KLYCGADGDMVPLGRCICSTGYEE 271

QY 249 VENGTVRCGPGSTFKANQGDCACTHCPINSRTTSEGATNCVCRNGYRADLDPMPCT 308  
Db 272 IEGS--CHACRPGFYKAPAGNTKCKPPHSLTYMEATSVQCCEKGYFRAEKDPPSMAC 329

QY 309 TIPSAPQAVISSVNETSLMLEWTPPRSGGREDLVYNIICKSCGSGRGACTRCGDNVOYA 368  
Db 330 RPPSAPRNVFNINETALILEWSPSDTGGKDLTYSVICKKGLDTSQCDGCGGLRFI 389

QY 369 PRQLGLEPRIYISDLLAHQTYTEIOAVNGVTDQSPSPQ-FASVNIITNQAPSASVI 427  
Db 390 PRHTGLNNSVIVLDFYSHVNYTFEIAMNGVSELS-FSPKPTAITVTTDQAPSLIGV 448

QY 428 MHQVSRVDSITLWSQDPDNGVILDELOYYEKELSE--YNATAIKSPNTVTVGLKAG 485  
Db 449 VRKDWASONSIALSWQAPAFSNGAILDYEIKYKEHEQULTYSSTRSKAPSVIITGLKPA 508

QY 486 AIYVQVARTVAGYGRYSGKMYFQTMTEAEYQTSIQEKLPLIGSSAAGLVFLIAVVI 545  
Db 509 TKYVFHVRVATATGYSGYSQKFEFETGDETSDMAEQQLVLTATAVGGFTLLVILTF 568

QY 546 AIVCNR-RGFERADSEYTDKLO-HYTSGHIT-PGMKIYIDPFTYEDPNEAVREFAKEIDI 602  
Db 569 FLITGRQWYIKAMKSEKRRNHLNGHLRFPFGIKTYIDPDYEDPSLAVHEFAKEIDP 628

QY 603 SCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTKQRDRFLSEASINGQFD 662  
Db 629 SRIRIERVIGAGEFGEVCSGLATPKCKREIPVAIKTLKGHMDRQRDRFLSEASINGQFD 688

QY 663 HPNVIHLEGVVTWT-----PVM 680  
Db 689 HPNIILEGVYTKRSPFAIGVEAFPCFLRAGFLNSIQAPHPVPGGSLPPRIAPGRPV 748

QY 681 IITFEMENGLSDFLRQNDQOFTVQLVGLRLGIAAGMKYLDAMVYVHRDLAARNILVNS 740  
Db 749 IIVVEYENGLSDFLRKHGHQHTVQLVGLRLGIAAGMKYLDAMVYVHRDLAARNILVNS 808

QY 741 NLVCKVSDGLSFLRLEDDTSDPTTYSALGKFPPIRWTAPEAIQYKFTSASDWSYGLVM 800  
Db 809 NLVCKVSDGLSFLRLEDD-PEAAVTTT-GGKIPIRWTAPEAIYKFTSASDWSYGLVM 866

QY 801 WEVMSYGERPYWDVNDQVINAIEDOYRLPPMDPCPSALHQLMDCWQRNHRPKFOI 860  
Db 867 WEVMSYGERPYWMSNQDVIILSEEGYRLPAPMGCPASLHQLMLHCWQKERNHRPKFTDI 926

QY 861 VNTLDKMRNPNSLKAMAPLSSGINLPDLRTIPDVTSTNTVDWLEAIKMGQYKESFAN 920  
Db 927 VSPDLKLRNPSALHTL--VEDILVMPESPGEVPEPLFTVVGDLNLSIKMGQYKNFEVA 984

QY 921 AGTSESDVVSQMMEDILRVGVTLAGHQKILNSIQVRAQMNQIQ 966  
Db 985 AGFTTDLIRMSIDDIRRIGVILIGHQRIRIVSSIQTLRLHMHQI 1030

RESULT 4  
US-09-922-138-2  
Sequence 2, Application US/09922138  
GENERAL INFORMATION:  
APPLICANT: Millennium Pharmaceuticals, Inc.  
APPLICANT: Meyers, Rachel  
APPLICANT: Silos-Santiago, Imaculada  
TITLE OF INVENTION: 16658, 14223 AND 16002, NOVEL HUMAN  
FILE REFERENCE: 38155-20030.00  
CURRENT APPLICATION NUMBER: US/09/922,138  
PRIOR FILING DATE: 2001-11-28  
PRIOR APPLICATION NUMBER: US 60/229,299  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 1130  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-922-138-2

Query Match 55.5%; Score 2837; DB 5; Length 1130;  
Best Local Similarity 53.6%; Pred. No. 3.9e-197;  
Matches 539; Conservative 167; Mismatches 240; Indels 60; Gaps 13;

QY 9 LMDSTTATLGMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKFIERRG 68  
Db 131 LDDTTVLGELGWKTYPLNGWDAITEMDEHNRPITHYQVCNVMEPNQNNWLRTNWSRDA 190

QY 69 ARIHVEKFSVRDCSSIPSPVPGSKETFNLYYEADPDSATKTFPNMNPWKVDTIA 128  
Db 191 AOKIYVEMKFTLRDCNSIPWLGTKETFNLFYMESDESHGKFKP-----NOYTKIDTIA 246

QY 129 ADESFQVDLGRVNMKINTEVRSGFVRSRSGFYLAFOYDYGCMSLIAVRVYRKCPRIIQ 188  
Db 247 ADESFQMDLGRILKLTREVGPIERKGFYLAFOYDYGCMSLIAVRVYRKCPRIIQ 306

QY 189 NGAIFQETLSGAESTSLVAARGSCIANAEVDVPILKYCNGDGEWLPVIGRCMCKAGFEA 248  
Db 307 NLAMFPDPIPRVDSLSLVEVRGSCVKAERDTP-KLYCGADGDMVPLGRCICSTGYEE 365

QY 249 VENGTVRCGPGSTFKANQGDCACTHCPINSRTTSEGATNCVCRNGYRADLDPMPCT 308  
Db 366 IEGS--CHACRPGFYKAPAGNTKCKPPHSLTYMEATSVQCCEKGYFRAEKDPPSMAC 423

QY 309 TIPSAPQAVISSVNETSLMLEWTPPRSGGREDLVYNIICKSCGSGRGACTRCGDNVOYA 368  
Db 424 RPPSAPRNVFNINETALILEWSPSDTGGKDLTYSVICKKGLDTSQCDGCGGLRFI 483

QY 369 PRQLGLEPRIYISDLLAHQTYTEIOAVNGVTDQSPSPQ-FASVNIITNQAPSASVI 427  
Db 484 PRHTGLNNSVIVLDFYSHVNYTFEIAMNGVSELS-FSPKPTAITVTTDQAPSLIGV 542

QY 428 MHQVSRVDSITLWSQDPDNGVILDELOYYEKELSE--YNATAIKSPNTVTVGLKAG 485  
Db 543 VRKDWASONSIALSWQAPAFSNGAILDYEIKYKEHEQULTYSSTRSKAPSVIITGLKPA 602

QY 486 AIYVQVARTVAGYGRYSGKMYFQTMTEAEYQTSIQEKLPLIGSSAAGLVFLIAVVI 545  
Db 603 TKYVFHVRVATATGYSGYSQKFEFETGDETSDMAEQQLVLTATAVGGFTLLVILTF 662

QY 546 AIVCNR-RGFERADSEYTDKLO-HYTSGHIT-PGMKIYIDPFTYEDPNEAVREFAKEIDI 602

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Db 663 FLITGRQWYIKAKMKSEKRRNLQNGHLRFPGIKTYIDPDTYEDPSLAVHEFAKIDP 722
Qy 603 SCVKIEQVIGAGEGECVSGHLKLPGRKEIFVAITKLSGVTEKORRDFLSEASIMQGF 662
Db 723 SRIRERVIGAGEGECVSGRLKTPGKREIPVAITKLSGVTEKORRDFLSEASIMQGF 782
Qy 663 HNVTHLEGVVTKST-----PVM 680
Db 783 HNIIRLEGVVTKSTFPAIGVEAFCPSFRAGFLNSIQAPHPVPGGSLPPRIAPGRPVM 842
Qy 681 IITEMWENGSLDSFLQRNDGFTVQLVGMRLGTAAGKYLADNMYHRDLAARNILVNS 740
Db 843 IIVVEWENGSLDSFLQRNDGFTVQLVGMRLGTAAGKYLADNMYHRDLAARNILVNS 902
Qy 741 NLVKVSDFLGRFLEDDTSDPTYSALGKFPPIRWTAPEAIQYRKFTSADVMSYGIYM 800
Db 903 NLVKVSDFLGRFLEDDTSDPTYSALGKFPPIRWTAPEAIQYRKFTSADVMSYGIYM 960
Qy 801 WEVMSYGERPYWDMNQDVINAIEQDYRLPPPMDCPSALHQLMDCWQKORNRHPRKGOI 860
Db 961 WEVMSYGERPYWDMNQDVINAIEQDYRLPPPMDCPSALHQLMDCWQKORNRHPRKFTDI 1020
Qy 861 VNTLDKMIKRNPSLAKAMAPLSSGILNPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFAN 920
Db 1021 VSFLDKLIIRNPSALHTL--VEDILVMPESPGEVPEYPLFVTVGDMWLSIKMGQYKNEVA 1078
Qy 921 AGTSPDVYSQMMEDILRVGYTLACHQKILNSIQVMAQNNQIQ 966
Db 1079 AGTTFDLISRMISIDDIRRIGVILIGHQRRIIVSSIQTLRLHMHQ 1124

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RESULT 5
US-09-971-708-3
; Sequence 3, Application US/09971708
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: Human EphA6 Gene and Polypeptide
; FILE REFERENCE: OCT 16U 102 R1
; CURRENT APPLICATION NUMBER: US/09/971,708
; CURRENT FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 1035
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-971-708-3

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Query Match 54.9%; Score 2811; DB 5; Length 1035;
Best Local Similarity 53.1%; Pred. No. 2.6e-195;
Matches 534; Conservative 165; Mismatches 248; Indels 58; Gaps 11;

Qy 9 LMDSTTAAELGMMVHPSPGWEVSGYVDENNTIRYQVNCVNFESSONWLRKFTERRG 68
Db 36 LDDTTVMGELGNKTYPLNGWDALTEDEHNRPIHTYQVNCVNFESSONWLRKFTERRG 95
Qy 69 AHRIVHEKFSVRDCSSIPSPGSKETENLYXYEADFSATKTFNPMNPNWVVDITIA 128
Db 96 AOKIYVEMKFTLRDCNIPWLVGCKFTFNLYYTESDEHGTKEP-----SQIKIDTIA 151
Qy 129 ADESGFQVLDGRVKNKINTEVRSGPYSGFYLAFQDYGGCMSLIAVAFYVKKCPRIQ 188
Db 152 ADESGFQVLDGRVKNKINTEVRSGPYSGFYLAFQDYGGCMSLIAVAFYVKKCPRIQ 211
Qy 189 NGATPQETLSAESTLSVAAGCAGIANAEVDVPIKLYCNGDCGEMWPIGRCMCKAGFEA 248
Db 212 SLAMPDPDIPRVDSSSLVEVRGCVKAAEERDTP-KLYCGADGDMWLVPLGRICSTGFE 270
Qy 249 VENGTVCRGCPGTFKANOAGDEACTHCPINRSTTSEGATNCVCRNGYIRADLDLPMPCT 308
Db 271 IEGS--CHACRPGFYKAFAGNATKSCPPHSSYVEATSVCHCEKGYFRAEKDPPSMACT 328

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Qy 309 TIPSAPQAVISSVNETSLMELWTPPRDSSGREDLVNIIICKSGRGAECTRCGNVOYA 368
Db 329 RPSAPRNVAFINETALILEWSPSDTGRKDLTVSVICKCKGLDTTQCECGGLRPI 388
Qy 369 PROGLTEPRIYISDLAHTQTFEIQAVNGVTDQSPFQSPQFASVNIITNOAPSASVIM 428
Db 389 PRHTGLNNSVVDVSHVNTFTEAMNGVSELSISPKPFTAITVTTVDHAPSILGMM 448
Qy 429 HQVSRIVDSTLWSOPDOPNGVILDYELQYKEKELSE--YNATAIKSPNTVTGKAGA 486
Db 449 RKMWASONSIALSWQAPAFNSGAILDIETKYEKEHEQIYTSSTRSKAPSVITGLKAT 508
Qy 487 IYVQVRAIVACVGRYSGKMYFQTMTEAEYQTSIQEKPLIIGSSAAGLVFLIAVVIA 546
Db 509 TYIFHIVRTATCYSGYSQKFEFETGDETSDMAAEGQILVIATAAVGGFTLLVILTF 568
Qy 547 IVGNR-RGFERASEYTDKLQ-HYTSCHIT-PGMKLYIDPFTVEDPNEAREFAKIDIS 603
Db 569 LITGRQWYIKAKMKSEKRRNLQNGHLRFPGIKTYIDPDTYEDPSLAVHEFAKIDPS 628
Qy 604 CVKTEOVIGAGEGECVSGHLKLPGRKEIFVAITKLSGVTEKORRDFLSEASIMQGF 663
Db 629 RIRLERVIGAGEGECVSGRLKTPGKREIPVAITKLSGVTEKORRDFLSEASIMQGF 688
Qy 664 PNVTHLEGVVTKST-----PVM 681
Db 689 PNIIRLEGVVTKSTFPAIGVEAFCPSFRAGFLNGIQAPHPVTAGGSLPPRIAPGRPVM 748
Qy 682 IITEMWENGSLDSFLQRNDGFTVQLVGMRLGTAAGKYLADNMYHRDLAARNILVNS 741
Db 749 VVEYWENGSLDSFLQRNDGFTVQLVGMRLGTAAGKYLADNMYHRDLAARNILVNS 808
Qy 742 LVCKVSDFLGRFLEDDTSDPTYSALGKFPPIRWTAPEAIQYRKFTSADVMSYGIYM 801
Db 809 LVCKVSDFLGRFLEDDTSDPTYSALGKFPPIRWTAPEAIQYRKFTSADVMSYGIYM 866
Qy 802 EVMSYGERPYWDMNQDVINAIEQDYRLPPPMDCPSALHQLMDCWQKORNRHPRKGOI 861
Db 867 EVMSYGERPYWDMNQDVINAIEQDYRLPPPMDCPSALHQLMDCWQKORNRHPRKFTDI 926
Qy 862 NTLDKMIKRNPSLAKAMAPLSSGILNPLDRTIPDYTSFNTVDEWLEAIKMGQYKESFANA 921
Db 927 SFLDKLIIRNPSALHTL--VEDILVMPESPGEVPEYPLFVTVGDMWLSIKMGQYKNEVA 984
Qy 922 GFTSPDVYSQMMEDILRVGYTLACHQKILNSIQVMAQNNQIQ 966
Db 985 GFTTFDLISRMISIDDIRRIGVILIGHQRRIIVSSIQTLRLHMHQ 1029

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RESULT 6
US-10-004-542-2
; Sequence 2, Application US/10004542
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Gerhardt, Brenda
; APPLICANT: Waake, D. Wade
; APPLICANT: Friedle, Carl Johan
; TITLE OF INVENTION: Novel Human Kinase and Polynucleotides
; FILE REFERENCE: LEX-0260-USA
; CURRENT APPLICATION NUMBER: US/10/004,542
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/243,893
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 942
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-004-542-2

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Query Match          42.2%; Score 2161.5; DB 6; Length 942;
Best Local Similarity 51.8%; Pred. No. 2.6e-148;
Matches 416; Conservative 133; Mismatches 200; Indels 57; Gaps 11;

Qy 9 LMDSTTAAELGMMVHPSPSGWEEVSGVDENMNTIRYQVCNVFESSONNWLTKFRRRG 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 LLDTTTTLGELGKWTPLNGMDAITENDEHNPIHYQVCNVFESSONNWLTKFRRRG 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 69 AHRHVKESVRCDSIPSPGSKETNLYYYEADFSATKTFNNMNMENPWVVDITA 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 AQLIYDMKFTLDCNSIPVLTGCTKTENLFYMESDESHGKFKP---NQYTKIDITA 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 129 ADEFSQVDLGGVMMKINTEVRSFGVPSRSGFLAFQDYGCGMSLIARVFRKCPRIIQ 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 ADESFQMDLGDRIILKLNTEIRVEGPIERKGYLAFQDYGACIALVSRVFRKCPFTVR 306
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 189 NGAIFOETLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRCMKAGFEA 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 307 NLAMFFDTIPRVDSLSLVEARGSCVKSABERDTP-KLYCGADGDLVPLGRICSTGIEE 365
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 249 VENGTVCRGCPSTFKANOGDEACTHCPINSTTSEGATNCVCRNGYYRADLDLPDMPCT 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 366 IEGS--CHACRGFYKAFAGNTKCKSPHSLTYMEATSVQCCEKGYPRAEKDPPSNACT 423
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 309 TIPSAPQAVISSNETSLMLEWTPPRDSGGREDLVYNIICKSGRGACRCGDNVQYA 368
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 RPPSAPRVVFNINETALILEWSPSPDGGRRKDLTYSVICKKGLDTSQCEDCGGGLRFI 483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 369 PROGLGTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQ-FASVNITTNQAAAPSASVI 427
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 484 PHTGLINNSVILDFVSHVNTYEIAENGVSLS-FSPKPTAITVTTDQDAPSLIGV 542
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 428 MHQVSRVDSITLSQSDQPNQVGLDYELQYKELSE--YNATAKSTNTVTGKAG 485
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 VRKDWASQNSIALSQAFNSGAILDYEIYKEHEQUTYSSTRKSPSVIITGLKPA 602
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 486 AIYVQVARTVAGRYGSKMYFQWTEAYOTSIOEKLPLIIGSSAAGLVFLIAVVI 545
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 TKYVPHIRVTRATGYSYGFEEFETDETSMAAEQGLIVIAATAVGGFTLLVILTLF 662
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 546 AIVCNR-RGFERADSEYTKLQ-HVTSCHIT-PCMKTYIDPFYEDPNEAVREFAKEIDI 602
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 FLITGRQWYIKAKKSEKRRNLQNGHURFPQIKTYIDPFYEDPSPSLAVHEFAKEIDP 722
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 603 SCVKIEQVIGAGEGVCSSHLKLPKREIFVAIKLKGSTYKQRDRDLSEASIMGQFD 662
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 723 SRIRIERVIGAGEGVCSSRLKTPKREIPVAIKLKGHMDRQRDRDLSEASIMGQFD 782
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 663 HPNVHLEGVVTKST-----PVM 680
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 783 HPNIIRLEGVVTKSRFPAIGVEAFCSFLRAGFLNSIQAPHPVPGGSLPPRIPAGRPVM 842
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 581 IITFEMENGLSFLRQNDQOFTVIQVGLMIRGIAAGMYLADMNVRDLAARNILVNS 740
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 843 IVVEYMENGLSFLRKHGHFTVIQVGLMIRGIAAGMYLSDMGVYVHDLAARNILVNS 902
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 741 NLVCKVSDGLSFLRLEDTSDDPYTS 766
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 903 NLVCKVSDGLSFLRLEDD-PEAAIYT 927
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-09-760-446A-1452
; Sequence 1452, Application US/09760446A
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT268
; CURRENT APPLICATION NUMBER: US/09760.446A
; CURRENT FILING DATE: 2000-01-16
; PRIOR APPLICATION NUMBER: 60/179,065

```

Query Match	35.0%;	Score 1793;	DB 5;	Length 406;
Best Local Similarity	82.2%;	Pred. No. 4e-122;		
Matches 337;	Conservative 33;	Mismatches 37;	Indels 4;	Gaps 1;
QY	561	YTDKLOHYTSHITPGMKIYIDPTTYEDPNEAVREFAKEIDISCKVIEOVIGAGEFGEVC	620	
Db	1	YTKLQOY-----IAPGMKVYIDPTTYEDPNEAVREFAKEIDNSCKVIEEVIGAGEFGEVC	56	
QY	621	SGHLKPGKREFLFAVIAKTLKSGYTEKORRDFLSEASIMGQFDHPNVIHLEGVVTKSTPVM	680	
Db	57	RGRLKOPGRRVFXAIAKTLKGYTERQRDFLSEASIMGQFDHPNIIRLEGVVTKSRPM	116	
QY	681	IIITEFMENGLDSFLRQNDGFTVIQLVGLMRGTAAGMKYLADNNYVHRDLAARNLLVNS	740	
Db	117	ILTEFMENCALDSFLRQNDGFTVIQLVGLMRGTAAGMKYLSENNYVHRDLAARNLLVNS	176	
QY	741	NLVCKYSDGLSRFLEDDTSDPTTYSALGGKFPRTWTAPEAIVKRYKFTSASDWSYGIYM	800	
Db	177	NLVCKYSDGLSRFLEDDSDPTTYSGLGKIPRTWTAPEAIVKRYKFTSASDWSYGIYM	236	
QY	801	WEVMSYGERPYWDMTNQDVINAIEQDYELPPMPCPSALHQLMDCWQKDRNHRPFGOI	860	
Db	237	WEVMSYGERPYWDMSNQDVINAIEQDYELPPMPCDPTALHQMDCWVRDNRNLPKFSQI	926	
QY	861	VNTLDKMRNPNSLKAMAPLSSGINPLIDRTIPDTSFNTVDEWLAEIAKMGQYKESFAN	920	



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PRIOR APPLICATION NUMBER: 60/249,218  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,208  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,213  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,212  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,207  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,245  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,244  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,217  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,211  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,215  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,264  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,214  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/249,297  
PRIOR FILING DATE: 2000-11-17  
PRIOR APPLICATION NUMBER: 60/232,400  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/231,242  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,081  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/232,080  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,414  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/231,244  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,064  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/233,063  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,397  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,399  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,401  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/241,808  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,826  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,786  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/241,221  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/246,475  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: 60/231,243  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 60/233,065  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: 60/232,398

Query Match 22.5%; Score 1150; DB 5; Length 270;  
Best Local Similarity 82.4%; Pred No. 8.5e-76;  
Matches 216; Conservative 24; Mismatches 20; Indels 2; Gaps 2;

QY 588 DPNEAVREFAKEIDISCVKIEQVIGAGEGVCVSHLPLPKGRKREIFVAIKTLKSGYTEKQ 647  
DB 1 DPNOAVHEFAKEIAESCITIERVIGAGEGVCVSHLPLPKGRKREIFVAIKTLKSGYTEKQ 60  
QY 648 RRDFLSEASIMGQFDHPNIIHLEGVVTKSTPYMIIIEFMENGSLDSFIRQNDGQFTVIQL 707

DB 61 RRDFLSEASIMGQFDHPNIIHLEGVVTKSTPYMIIIEFMENGSLDSFIRQNDGQFTVIQL 120  
QY 708 VGMURGIAGMKYLAADNMYVRDLAARNILVNSNLVCKVSDFGLSRFLSDPTSDPTSA 767  
DB 121 VGMURGISAGMKYLSMDGYVHRDLAARNILVNSNLVCKVSDFGLSRFLSDPTSDPTSA 179  
QY 768 LGGKFPRTWTAPEAIQYRKFTSASDVNSYGIYVMEVMSYGERPYWMTNODVINAIEODY 827  
DB 180 -GGKIPRTWTAPEAIQYRKFTSASDVNSYGIYVMEVMSYGERPYWMTNODVINAIEODY 238  
QY 828 RLPPPMDCPSALHQLMLDCWOK 849  
DB 239 RLPPPMDCPSALHQLMLDCWOK 260  
RESULT 9  
US-09-760-446A-1538  
; Sequence 1538, Application US/09760446A  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT268  
; CURRENT APPLICATION NUMBER: US/09760,446A  
; PRIOR FILING DATE: 2000-01-16  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/225,757  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/226,868  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/216,647  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,267  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/216,880  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: 60/225,270  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/251,869  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/235,834  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/234,274  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/234,223  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/228,924  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/224,518  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,369  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/224,519  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,964  
; PRIOR FILING DATE: 2000-07-26

1	PRIOR FILING DATE: 2000-08-14
2	PRIOR APPLICATION NUMBER: 60/235,836
3	PRIOR FILING DATE: 2000-09-27
4	PRIOR APPLICATION NUMBER: 60/230,438
5	PRIOR FILING DATE: 2000-09-06
6	PRIOR APPLICATION NUMBER: 60/215,135
7	PRIOR FILING DATE: 2000-06-30
8	PRIOR APPLICATION NUMBER: 60/235,266
9	PRIOR FILING DATE: 2000-08-14
10	PRIOR APPLICATION NUMBER: 60/249,218
11	PRIOR FILING DATE: 2000-11-17
12	PRIOR APPLICATION NUMBER: 60/249,208
13	PRIOR FILING DATE: 2000-11-17
14	PRIOR APPLICATION NUMBER: 60/249,213
15	PRIOR FILING DATE: 2000-11-17
16	PRIOR APPLICATION NUMBER: 60/249,212
17	PRIOR FILING DATE: 2000-11-17
18	PRIOR APPLICATION NUMBER: 60/249,207
19	PRIOR FILING DATE: 2000-11-17
20	PRIOR APPLICATION NUMBER: 60/249,245
21	PRIOR FILING DATE: 2000-11-17
22	PRIOR APPLICATION NUMBER: 60/249,244
23	PRIOR FILING DATE: 2000-11-17
24	PRIOR APPLICATION NUMBER: 60/249,217
25	PRIOR FILING DATE: 2000-11-17
26	PRIOR APPLICATION NUMBER: 60/249,211
27	PRIOR FILING DATE: 2000-11-17
28	PRIOR APPLICATION NUMBER: 60/249,215
29	PRIOR FILING DATE: 2000-11-17
30	PRIOR APPLICATION NUMBER: 60/249,264
31	PRIOR FILING DATE: 2000-11-17
32	PRIOR APPLICATION NUMBER: 60/249,214
33	PRIOR FILING DATE: 2000-11-17
34	PRIOR APPLICATION NUMBER: 60/249,297
35	PRIOR FILING DATE: 2000-11-17
36	PRIOR APPLICATION NUMBER: 60/232,400
37	PRIOR FILING DATE: 2000-09-14
38	PRIOR APPLICATION NUMBER: 60/231,242
39	PRIOR FILING DATE: 2000-09-08
40	PRIOR APPLICATION NUMBER: 60/232,081
41	PRIOR FILING DATE: 2000-09-08
42	PRIOR APPLICATION NUMBER: 60/232,080
43	PRIOR FILING DATE: 2000-09-08
44	PRIOR APPLICATION NUMBER: 60/231,414
45	PRIOR FILING DATE: 2000-09-08
46	PRIOR APPLICATION NUMBER: 60/231,244
47	PRIOR FILING DATE: 2000-09-08
48	PRIOR APPLICATION NUMBER: 60/233,064
49	PRIOR FILING DATE: 2000-09-14
50	PRIOR APPLICATION NUMBER: 60/233,063
51	PRIOR FILING DATE: 2000-09-14
52	PRIOR APPLICATION NUMBER: 60/232,397
53	PRIOR FILING DATE: 2000-09-14
54	PRIOR APPLICATION NUMBER: 60/232,399
55	PRIOR FILING DATE: 2000-09-14
56	PRIOR APPLICATION NUMBER: 60/232,401
57	PRIOR FILING DATE: 2000-09-14
58	PRIOR APPLICATION NUMBER: 60/241,808
59	PRIOR FILING DATE: 2000-10-20
60	PRIOR APPLICATION NUMBER: 60/241,826
61	PRIOR FILING DATE: 2000-10-20
62	PRIOR APPLICATION NUMBER: 60/241,786
63	PRIOR FILING DATE: 2000-10-20
64	PRIOR APPLICATION NUMBER: 60/241,221
65	PRIOR FILING DATE: 2000-10-20
66	PRIOR APPLICATION NUMBER: 60/246,475
67	PRIOR FILING DATE: 2000-11-08
68	PRIOR APPLICATION NUMBER: 60/231,243
69	PRIOR FILING DATE: 2000-09-08
70	PRIOR APPLICATION NUMBER: 60/233,065
71	PRIOR FILING DATE: 2000-09-14
72	PRIOR APPLICATION NUMBER: 60/232,398

```

Query Match          21.68;  Score 1103.5;  DB 5;  Length 277;
Best Local Similarity 65.8%;  Pred. No. 2.1e-72;
Matches 214;  Conservative 26;  Mismatches 24;  Indels 61;  Gaps 1;

QY  488  YFQVARTVAGYGRYSKMYFQMTAEAYQTSIQEKPLPLIIGSSAGLVFLIANVVIAI 547
DB 3     YLVQVRRSEAGYGFQGHHSQTOLD-----GTVYIDPFTYEDNPNAVREFAKEIDVSVKI 61
QY  548  VCNRRGFERADSEYTDKLQHYTSGHITFCMKIYIDPFTYEDNPNAVREFAKEIDVSVKI 607
DB 30    ------GTVYIDPFTYEDNPNAVREFAKEIDVSVKI 61
QY  608  EQVIGAGEGECVCSGHLKLPGRKEIFVAIKTLKSGYTEKQRDRFLSEASIMGQFDHPNVI 667
DB 62    EEVIGAGEGECVGRGLKAPGRKESCVAIKTLKSGYTEKQRDRFLSEAS:MGQFEHPNII 121
QY  668  HLEGVTKSPVMIIITFEMENGLSFLRQNDGQFTVQLVCMRLGRTAAIMKYLADNMYV 727
DB 122   RLEGVTVNSPMVILITFEMENGALDSFLRLNDGQFTVQLVCMRLGRTASMRXLAEMSYV 181
QY  728  HRDLAARNILVNSNLCKVSDGSLRFLEDDFTYTSALGGKFPRTWTAPEAIOYRKF 787
DB 182   HRDLAARNILVNSNLCKVSDGSLRFLEENSDFTYTSALGGKIPRTWTAPEAIAFRKF 241
QY  788  TSASDWSYGIVMWVMSYGERPYW 812
DB 242   TSASDWSYGIVMWVMSYGERPYW 266

RESULT 10
US-09-760-446A-2141
; Sequence 2141, Application US/09760446A
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ68
; CURRENT APPLICATION NUMBER: US/09760,446A
; CURRENT FILING DATE: 2000-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274

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; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
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; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,245
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,398

```

```

Query Match 16.1%; Score 822; DB 5; Length 189;
Best Local Similarity 79.6%; Pred. No. 3e-52;
Matches 152; Conservative 21; Mismatches 16; Indels 2; Gaps 2;

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QY 682 ITEFMENGLDSEFLRQNDGQFTVQLVGLMRLGTAAGKYLADNMYVHRDLAARNILVNSN 741
Db 1 VTEYMENGLDSEFLRQNDGQFTVQLVGLMRLGTAAGKYLADNMYVHRDLAARNILVNSN 60
QY 742 LVCKVSDFGSLRLEDDTSDPTYSALGKGFPIRTWTAPEAIOYRKFTSASDVNSYGIYMW 801
Db 61 LVCKVSDFGSLRLEDD-PEAYTTR-GGKIPRTWTAPEAIAFRKFTSASDVNSYGIYMW 118
QY 802 EVMSYGERPYWMTNODVINAIEDQYRLPPMDPCPSALHQLMDCWQKDRNHRPKFGQIV 861
Db 119 EVMSYGERPYWMTNODVINAIEDQYRLPPMDPCPSALHQLMDCWQKDRNHRPKFGQIV 178
QY 862 NTLDKMIRNPN 872
Db 179 NMLDKLIRNPS 189

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RESULT 11

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PCT-US01-30539-4
; Sequence 4, Application PC/TUS0130539
; GENERAL INFORMATION:
; APPLICANT: PE CORPORATION (NY)
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01156PCT
; CURRENT APPLICATION NUMBER: PCT/US01/30539
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 09/799,345
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Rattus norvegicus
PCT-US01-30539-4

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Query Match 15.38; Score 784.5; DB 1; Length 265;
Best Local Similarity 56.78; Pred. No. 2.5e-49;
Matches 144; Conservative 48; Mismatches 55; Indels 7; Gaps 3;

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QY 3 AAVEETLMDSTATAELGWMVHPSPSGWEEVSGYDENNMNTIRTYQVCNVPSSONNLRTK 62
Db 17 AAKEVLLDLSKAQTELEWISSPPSGWEEISGLDENYTPRTYQVCNVPSSONNLRTN 76
QY 63 FIRRGARHRTVENKFSVRDCCSIPSPSGWEEISGLDENYTPRTYQVCNVPSSONNLRTN 122
Db 77 WISGNAQRIFVELKFTLRDCNSLPGVLGTCETFNLYYETDYD---TGRNIRENLV 132
QY 123 KVDITIAADESFQVDLGGVRVMTKINTVRSRPSRSGVLAQDYGGCSLTAVRFYRK 182
Db 133 KIDTIADESFTQDGLGERKMKLNTVEIRGLSKGKGYLAQDYGGCSLTAVRFYRK 192
QY 183 CPRIQNGAIFQETLSGAESTSLVAARGSCIANA-EVDVPIKLYCNGDGEWLVPITGRCM 241

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ORGANISM: Mus musculus  
PCT-US01-30539-6  
Query Match 15.3%; Score 783.5; DB 1; Length 265;  
Best Local Similarity 56.3%; Pred. No. 3e-49; Indels 7; Gaps 3;  
Matches 143; Conservative 49; Mismatches 55;  
QY 3 AAVEETIMDSATTATAELGWMVHPSPSGWEVSGYDENMNTIRTYQVCNVPFESSQNWLRTK 62  
Db 17 AAKEVLLDSKAQQTLEWISSPPSGWEEISGLDENYTPRTYQVCQVMEPNQNNWLRTN 76  
QY 63 FIRRGAHRHIVEMKFSVRDCSIPSPGSKETFLNYEADFSATKTFNWMENPV 122  
Db 77 WISGNAQRIFVELKTLRDCNSLPGVLGTCKETFLNYEADFSATKTFNWMENPV 132  
QY 123 KVDITIADESFSQVDLGGVRMKNTEVRSFGVPSRSGFYLAFOYDYGCCMSLIAVRVYRK 182  
Db 133 KIDTIAADESFTQDGLGERMKNTEVREIGPLSKGKGYLAFOYDVGACIALYSVKYYKK 192  
QY 183 CPRIQNGAIFOETLSGAESTSLVAARGSCIANA-EVDVPIKLYCNGDGWLVPIGRM 241  
Db 193 CWTIVENLAVFPDVTGSEFSSLVVEVRGTCVSSAAEEAENSPRMHCSAEGEWLVPIGKCI 252  
QY 242 CKAGFEAVENGTV 255  
Db 253 CKAGYQ--QKGDTC 264  
RESULT 14  
US-10-004-542-4  
; Sequence 4, Application US/10004542  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Yi  
; APPLICANT: Nepomnichy, Boris  
; APPLICANT: Gerhardt, Brenda  
; APPLICANT: Walke, D, Wade  
; APPLICANT: Fridele, Carl Johan  
; TITLE OF INVENTION: Novel Human Kinase and Polynucleotides  
; TITLE OF INVENTION: Encoding the Same  
; FILE REFERENCE: LEX-0260-USA  
; CURRENT APPLICATION NUMBER: US/10/004,542  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/243,893  
; PRIOR FILING DATE: 2000-10-27  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-004-542-4  
Query Match 15.1%; Score 771; DB 6; Length 308;  
Best Local Similarity 55.9%; Pred. No. 2.9e-48; Indels 46; Gaps 5;  
Matches 162; Conservative 36; Mismatches 46;  
QY 522 QEKPLIIGSSAAGLVFLIATVAVVIAVGNR-RGFERADSEYTDKIQ-HYTSGHIT-PGKM 578  
Db 5 QGQILVATAAAGVFTLLVILLITLITRCQWYIKAKMKSEKRRNLQNGHLRFPPIK 64  
QY 579 IYIDPTFYEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVSGHKLPGKREIFVAIKT 638  
Db 65 TYIDPTFYEDPNSLAVHEFAKEIDPSRIRIERVIGAGEFGEVSGRLKTPGKREIFVAIKT 124  
QY 639 LKSGYTEKORRDFLSEASIMGQFDHPNVHLEGVYTKST----- 677  
Db 125 LKGGHMDRQRDFLREASIMGQFDHPNIIRLEGVYTKRSPFPAIGVAFPCFSLRAGFLNS 184  
QY 678 -----PVAITEFMENGSLDSFLRQNDQFTVIQYVGLMRLGIAA 716  
Db 185 IQAPHPVPGGSLPPIPRAGRPVMIIVVEYNGSLDSFLRKHGHFTVIQYVGLMRLGIAA 244

ORGANISM: Mus musculus  
PCT-US01-30539-5  
Query Match 15.3%; Score 783.5; DB 1; Length 265;  
Best Local Similarity 56.3%; Pred. No. 3e-49; Indels 7; Gaps 3;  
Matches 143; Conservative 49; Mismatches 55;  
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Db 17 AAKEVLLDSKAQQTLEWISSPPSGWEEISGLDENYTPRTYQVCQVMEPNQNNWLRTN 76  
QY 63 FIRRGAHRHIVEMKFSVRDCSIPSPGSKETFLNYEADFSATKTFNWMENPV 122  
Db 77 WISGNAQRIFVELKTLRDCNSLPGVLGTCKETFLNYEADFSATKTFNWMENPV 132  
QY 123 KVDITIADESFSQVDLGGVRMKNTEVRSFGVPSRSGFYLAFOYDYGCCMSLIAVRVYRK 182  
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QY 183 CPRIQNGAIFOETLSGAESTSLVAARGSCIANA-EVDVPIKLYCNGDGWLVPIGRM 241  
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Db 253 CKAGYQ--QKGDTC 264  
RESULT 13  
PCT-US01-30539-6  
; Sequence 6, Application PC/TUS0130539  
; GENERAL INFORMATION:  
; APPLICANT: PE CORPORATION (NY)  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001156PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/30539  
; CURRENT FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: 09/799,345  
; PRIOR FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Mus musculus  
PCT-US01-30539-5  
Query Match 15.3%; Score 783.5; DB 1; Length 265;  
Best Local Similarity 56.3%; Pred. No. 3e-49; Indels 7; Gaps 3;  
Matches 143; Conservative 49; Mismatches 55;  
QY 3 AAVEETIMDSATTATAELGWMVHPSPSGWEVSGYDENMNTIRTYQVCNVPFESSQNWLRTK 62  
Db 17 AAKEVLLDSKAQQTLEWISSPPSGWEEISGLDENYTPRTYQVCQVMEPNQNNWLRTN 76  
QY 63 FIRRGAHRHIVEMKFSVRDCSIPSPGSKETFLNYEADFSATKTFNWMENPV 122  
Db 77 WISGNAQRIFVELKTLRDCNSLPGVLGTCKETFLNYEADFSATKTFNWMENPV 132  
QY 123 KVDITIADESFSQVDLGGVRMKNTEVRSFGVPSRSGFYLAFOYDYGCCMSLIAVRVYRK 182  
Db 133 KIDTIAADESFTQDGLGERMKNTEVREIGPLSKGKGYLAFOYDVGACIALYSVKYYKK 192  
QY 183 CPRIQNGAIFOETLSGAESTSLVAARGSCIANA-EVDVPIKLYCNGDGWLVPIGRM 241  
Db 193 CWTIVENLAVFPDVTGSEFSSLVVEVRGTCVSSAAEEAENSPRMHCSAEGEWLVPIGKCI 252  
QY 242 CKAGFEAVENGTV 255  
Db 253 CKAGYQ--QKGDTC 264  
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; Sequence 6, Application PC/TUS0130539  
; GENERAL INFORMATION:  
; APPLICANT: PE CORPORATION (NY)  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001156PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/30539  
; CURRENT FILING DATE: 2001-03-06  
; PRIOR APPLICATION NUMBER: 09/799,345  
; PRIOR FILING DATE: 2001-03-06  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 265  
; TYPE: PRT

QY 717 GMKYLADMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTYS 766  
 Db 245 GMKYLSDMGVYHRDLAARNILVNSLVCKVSDFGLSRLEDD-PEAAYTT 293

RESULT 15

US-09-971-708-5  
 ; Sequence 5, Application US/09971708  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Origene Technologies, Inc  
 ; TITLE OF INVENTION: Human EphA6 Gene and Polypeptide  
 ; FILE REFERENCE: OGT 160 102 R1  
 ; CURRENT APPLICATION NUMBER: US/09/971.708  
 ; CURRENT FILING DATE: 2001-10-09  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 334  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: MISC FEATURE  
 ; LOCATION: (3)-(24)  
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 US-09-971-708-5

Query Match 15.1%; Score 771; DB 5; Length 334;  
 Best Local Similarity 55.9%; Pred. No. 3.3e-48;  
 Matches 162; Conservative 36; Mismatches 46; Indels 46; Gaps 5;  
 QY 522 QEKPLITGSSAAGLVFLIAVVIACNR-RGPERADSEYTDKIQ-HYTSGHIT-PGMK 578  
 Db 31 QGQILVITATAVGGFTLLVILTLFLLITGRQWYKAKMKSEKRRNHLQNGHLRFPQIK 90  
 QY 579 IYIDPFTYEDPNEAVREFAKEIDISCVKIQVIGAGEFGEVCSGHLKLPCKREIFVAIKT 638  
 Db 91 TYIDPDTYEDPSLAVHEFAKEIDPSRIRIERVIGAGEFGEVCSGRLKTPGKREIPVAIKT 150  
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 Db 151 LKGGHMDRQRDRFLREASINGQFDHPNIIIRLEGVVTYKRSFPAIGVEAFCEPSFLRAGFLNS 210  
 QY 678 -----PWAITFENGSLDSFLRQNDGQFTVIQLVGMRLGIAA 716  
 Db 211 IQAPHPVPGGSLPPRIIPAGRPYHIVVEYMENGSLDSFLRKHGDFTVIQLVGMRLGIAA 270  
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 Db 271 GMKYLSDMGVYHRDLAARNILVNSLVCKVSDFGLSRLEDD-PEAAYTT 319

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run On: February 1, 2002, 09:53:00 ; Search time 192.18 Seconds  
(without alignments)  
1401.433 Million cell updates/sec

Title: US-09-378-759-11  
Perfect score: 5116  
Sequence: 1 LLAAVEETLMDTTATAEIG.....ILNSTQVMRAQNNQIQSVEV 970

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5116	100.0	970	8	US-08-449-645-11
2	5116	100.0	970	11	US-08-702-367-11
3	5116	100.0	970	17	US-09-378-759-11
4	5082	99.3	994	6	US-08-235-407-2
5	5082	99.3	994	11	US-08-727-463-2
6	5082	99.3	994	11	US-08-727-463-2
7	5082	99.3	994	11	US-08-730-700-2
8	5082	99.3	994	11	US-08-730-700A-2
9	5082	99.3	994	20	US-09-621-595-2

10	3901.5	76.3	990	15	US-09-194-755A-7	Sequence 7, Appl1
11	3735	73.0	1009	3	US-07-861-390D-6	Sequence 6, Appl1
12	3632.5	71.0	998	8	US-08-449-645-20	Sequence 20, Appl
13	3632.5	71.0	998	11	US-08-702-367-20	Sequence 20, Appl
14	3632.5	71.0	998	17	US-09-378-759-20	Sequence 20, Appl
15	3632.5	71.0	1007	1	PCT-US01-03800A-2273	Sequence 2273, Ap
16	3631.5	71.0	999	24	US-60-201-702-172	Sequence 211, App
17	3590.5	70.2	993	19	US-09-558-340-1	Sequence 172, App
18	3545.5	69.3	961	24	US-60-200-366-202	Sequence 202, App
19	3545.5	69.3	961	24	US-60-201-702-165	Sequence 165, App
20	3520.5	68.8	951	24	US-60-205-421-278	Sequence 278, App
21	3470	67.8	908	24	US-60-200-366-211	Sequence 211, App
22	3470	67.8	908	24	US-60-201-702-161	Sequence 161, App
23	3448.5	67.4	911	24	US-60-201-702-173	Sequence 173, App
24	3401	66.5	954	24	US-60-205-421-275	Sequence 275, App
25	3354	65.6	947	24	US-60-201-702-166	Sequence 166, App
26	3341.5	65.3	1002	15	US-09-194-755A-6	Sequence 6, Appl1
27	3292.5	64.4	889	24	US-60-201-702-162	Sequence 162, App
28	3289.5	64.3	905	24	US-60-205-421-289	Sequence 289, App
29	3031	59.2	953	21	US-09-751-389-7	Sequence 30, Appl
30	3031	59.2	967	17	US-09-378-759-30	Sequence 15, Appl
31	3031	59.2	986	8	US-08-449-645-15	Sequence 15, Appl
32	3031	59.2	986	11	US-08-702-367-15	Sequence 13, Appl
33	3031	59.2	986	17	US-09-378-759-15	Sequence 13, Appl
34	3031	59.2	991	8	US-08-449-645-13	Sequence 15, Appl
35	3031	59.2	991	11	US-08-702-367-13	Sequence 13, Appl
36	3031	59.2	991	17	US-09-378-759-13	Sequence 13, Appl
37	3031	59.2	991	22	US-09-823-187-44	Sequence 44, Appl
38	3031	59.2	997	1	PCT-US01-08631-36048	Sequence 36048, A
39	3031	59.2	1026	1	PCT-US01-08631-53290	Sequence 53290, A
40	3026.5	59.2	993	22	US-09-823-187-39	Sequence 39, Appl
41	3026.5	59.2	993	22	US-09-823-187-41	Sequence 41, Appl
42	3024	59.1	1104	8	US-08-446-648-36	Sequence 36, Appl
43	3024	59.1	1104	11	US-08-770-449-36	Sequence 36, Appl
44	3016	59.0	998	8	US-08-449-645-17	Sequence 17, Appl
45	3016	59.0	998	11	US-08-702-367-17	Sequence 17, Appl

## ALIGNMENTS

RESULT 1

US-08-449-645-11

; Sequence 11, Application US/08449645

; GENERAL INFORMATION:

; APPLICANT: Fox, Gary M.

; APPLICANT: Welch, Andrew A.

; APPLICANT: Jing, Shugan

; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

; TITLE OF INVENTION: Kinases

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Patent Operations/RBW

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,645

; FILING DATE: May 24, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-287-A

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 970 amino acids

; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-449-645-11

Query Match	100.0%;	Score 5116;	DB 8;	Length 970;
Best Local Similarity	100.0%;	Pred. NO. 0;		
Matches 970;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

  

Qy	1	LAAVEETLMDSTTATAELGWNVHPSPGWEVSGYDENNMRTIRYQVCNVFESSNNWLR	60
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Qy	61	TKFIRRGARHIVEMKFSVRDCSSIPSPGCKETFNLYYEADFDSATKTFPNWENP	120
Db	61	TKFIRRGARHIVEMKFSVRDCSSIPSPGCKETFNLYYEADFDSATKTFPNWENP	120
Qy	121	WKVDTIAADESFQVDLGGVRVKINTVERSGPVSRGFLAFQDYGCMGLIAVRVY	180
Db	121	WKVDTIAADESFQVDLGGVRVKINTVERSGPVSRGFLAFQDYGCMGLIAVRVY	180
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Qy	301	DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR	360
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Qy	601	DISCVKIEQVIGAGEGVCVSGHKLPGKREIFVAIKTLKSGYTEKQKRDFTSEASIMQ	660
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Qy	661	FDPNVIHLGCVTKSTPMIITEFENGSLDSFLQNDQGFVIOLVGMLRGIAAGMKY	720
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Qy	841	QMLDCHQKDRNHRPKFGQIVNTLDKMRNPNSIKAPALSSGINPLDRTIPDVTSEN	900
Db	841	QMLDCHQKDRNHRPKFGQIVNTLDKMRNPNSIKAPALSSGINPLDRTIPDVTSEN	900
Qy	901	TVDEWLEAIKMGQYKESFANAGETSFQVVSOMMEDILRVGVTLGAGHQKILNSIQVMA	960
Db	901	TVDEWLEAIKMGQYKESFANAGETSFQVVSOMMEDILRVGVTLGAGHQKILNSIQVMA	960

Qy 961 QMNOIOSVEV 970  
 Db 961 QMNOIOSVEV 970  
 RESULT 2  
 US-08-702-367-11  
 ; Sequence 11, Application US/08702367  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fox, Gary M.  
 ; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine  
 ; TITLE OF INVENTION: Kinases  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Amgen Patent Operations/RBW  
 ; STREET: 1840 Dehavilland Drive  
 ; CITY: Thousand Oaks  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 91320  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION NUMBER: US/08/702,367  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/229,509  
 ; FILING DATE: 15-APR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Winter, Robert B.  
 ; REFERENCE/DOCKET NUMBER: A-287  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 970 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-702-367-11

Query Match 100.0%; Score 5116; DB 11; Length 970;  
 Best Local Similarity 100.0%; Pred. NO. 0;  
 Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	LAAVEETLMDSTTATAELGWNVHPSPGWEVSGYDENNMRTIRYQVCNVFESSNNWLR	60
Db	1	LAAVEETLMDSTTATAELGWNVHPSPGWEVSGYDENNMRTIRYQVCNVFESSNNWLR	60
Qy	61	TKFIRRGARHIVEMKFSVRDCSSIPSPGCKETFNLYYEADFDSATKTFPNWENP	120
Db	61	TKFIRRGARHIVEMKFSVRDCSSIPSPGCKETFNLYYEADFDSATKTFPNWENP	120
Qy	121	WKVDTIAADESFQVDLGGVRVKINTVERSGPVSRGFLAFQDYGCMGLIAVRVY	180
Db	121	WKVDTIAADESFQVDLGGVRVKINTVERSGPVSRGFLAFQDYGCMGLIAVRVY	180
Qy	181	RKCPRIQNGALFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGR	240
Db	181	RKCPRIQNGALFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGR	240
Qy	241	MCAGFEAVENTVCGCPGSGTFFKANQDEACTHCPINSRTTSEGATNCVCNGYRADL	300
Db	241	MCAGFEAVENTVCGCPGSGTFFKANQDEACTHCPINSRTTSEGATNCVCNGYRADL	300
Qy	301	DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR	360
Db	301	DPLDMPCTTIPSAPOAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR	360

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QY 361 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQFASVNTTNOA 420
Db 361 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQFASVNTTNOA 420
QY 421 APSAVSIMHQVSTVDSITLSWSQDPOPNVILDELYQYKELSEYNATAIKSPNTVT 480
Db 421 APSAVSIMHQVSTVDSITLSWSQDPOPNVILDELYQYKELSEYNATAIKSPNTVT 480
QY 481 GLKAGAIYVFOVRARTVAGYGRYSGKMYFQTMTEAEYQTSIQEKLPLIGSSAAGLVFLI 540
Db 481 GLKAGAIYVFOVRARTVAGYGRYSGKMYFQTMTEAEYQTSIQEKLPLIGSSAAGLVFLI 540
QY 541 AVVYIAIVCNRRGFERADSEYTDKLQHYTSGHITPGMKIYIDPFTYEDPNEAVREFAKEI 600
Db 541 AVVYIAIVCNRRGFERADSEYTDKLQHYTSGHITPGMKIYIDPFTYEDPNEAVREFAKEI 600
QY 601 DISCVKIEQVIGAGEGECVSGHKLPGKREIFVAIKTLKSGYTEKQRDRDLSEASIMQ 660
Db 601 DISCVKIEQVIGAGEGECVSGHKLPGKREIFVAIKTLKSGYTEKQRDRDLSEASIMQ 660
QY 661 FDHPNVIHLEGVVTKSTPVMIIITEPMENGSLDSFLRQNDGQFTVIQLVGLRGIAAGMKY 720
Db 661 FDHPNVIHLEGVVTKSTPVMIIITEPMENGSLDSFLRQNDGQFTVIQLVGLRGIAAGMKY 720
QY 721 LADMNVYHRDLAARNILVNSNLVKVDFGLSRLEDDTSDPTVTSALGGKFPRIWTAPE 780
Db 721 LADMNVYHRDLAARNILVNSNLVKVDFGLSRLEDDTSDPTVTSALGGKFPRIWTAPE 780
QY 781 AIQYRKFTSASDVMSYGIWMVEVMSYGERPYWDMTNQDVINAIEDYRLPPMDPCPSALH 840
Db 781 AIQYRKFTSASDVMSYGIWMVEVMSYGERPYWDMTNQDVINAIEDYRLPPMDPCPSALH 840
QY 841 QLMDCWQKDRHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPLDRTIPDYTSFN 900
Db 841 QLMDCWQKDRHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPLDRTIPDYTSFN 900
QY 901 TVDEWLEAIKMGQYKESFANAGFTSFQVVSOMMEDILRVGVTLAGHQKILNSIQVMRA 960
Db 901 TVDEWLEAIKMGQYKESFANAGFTSFQVVSOMMEDILRVGVTLAGHQKILNSIQVMRA 960
QY 961 QMNOIQSVEV 970
Db 961 QMNOIQSVEV 970

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RESULT 3
US-09-378-759-11
; Sequence 11, Application US/09378759
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
; TITLE OF INVENTION: Kinases
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,759
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

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; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-378-759-11

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Query Match 100.0%; Score 5116; DB 17; Length 970;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 970; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LLAARETLMDSITATAELGWMVHPSPSGWEEVSGVDENNMNTIRTYQVCNVFSSQNNMLR 60
Db 1 LLAARETLMDSITATAELGWMVHPSPSGWEEVSGVDENNMNTIRTYQVCNVFSSQNNMLR 60
QY 61 TKFIRRRGAHRIHVENKFSVRDCSSIPSPGSKETENLYYEADFDSATKTFPNNMENP 120
Db 61 TKFIRRRGAHRIHVENKFSVRDCSSIPSPGSKETENLYYEADFDSATKTFPNNMENP 120
QY 121 WKVVDITAADESFQVDLGGVRVNMKINTEVRSFSPVSRSGFYLAQDYGGCMLTAIVRFY 180
Db 121 WKVVDITAADESFQVDLGGVRVNMKINTEVRSFSPVSRSGFYLAQDYGGCMLTAIVRFY 180
QY 181 RKPRIQNGALFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRC 240
Db 181 RKPRIQNGALFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGRC 240
QY 241 MCKAGFEAVENGTVCGCPSTGTFKANQDEACTHCPINSRITTSAGATNCVCRNYYRADL 300
Db 241 MCKAGFEAVENGTVCGCPSTGTFKANQDEACTHCPINSRITTSAGATNCVCRNYYRADL 300
QY 301 DPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSSGREDLVYNIICKSGSGRGACTR 360
Db 301 DPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSSGREDLVYNIICKSGSGRGACTR 360
QY 361 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQFASVNTTNOA 420
Db 361 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPSPQFASVNTTNOA 420
QY 421 APSAVSIMHQVSTVDSITLSWSQDPOPNVILDELYQYKELSEYNATAIKSPNTVT 480
Db 421 APSAVSIMHQVSTVDSITLSWSQDPOPNVILDELYQYKELSEYNATAIKSPNTVT 480
QY 481 GLKAGAIYVFOVRARTVAGYGRYSGKMYFQTMTEAEYQTSIQEKLPLIGSSAAGLVFLI 540
Db 481 GLKAGAIYVFOVRARTVAGYGRYSGKMYFQTMTEAEYQTSIQEKLPLIGSSAAGLVFLI 540
QY 541 AVVYIAIVCNRRGFERADSEYTDKLQHYTSGHITPGMKIYIDPFTYEDPNEAVREFAKEI 600
Db 541 AVVYIAIVCNRRGFERADSEYTDKLQHYTSGHITPGMKIYIDPFTYEDPNEAVREFAKEI 600
QY 601 DISCVKIEQVIGAGEGECVSGHKLPGKREIFVAIKTLKSGYTEKQRDRDLSEASIMQ 660
Db 601 DISCVKIEQVIGAGEGECVSGHKLPGKREIFVAIKTLKSGYTEKQRDRDLSEASIMQ 660
QY 661 FDHPNVIHLEGVVTKSTPVMIIITEPMENGSLDSFLRQNDGQFTVIQLVGLRGIAAGMKY 720
Db 661 FDHPNVIHLEGVVTKSTPVMIIITEPMENGSLDSFLRQNDGQFTVIQLVGLRGIAAGMKY 720
QY 721 LADMNVYHRDLAARNILVNSNLVKVDFGLSRLEDDTSDPTVTSALGGKFPRIWTAPE 780
Db 721 LADMNVYHRDLAARNILVNSNLVKVDFGLSRLEDDTSDPTVTSALGGKFPRIWTAPE 780
QY 781 AIQYRKFTSASDVMSYGIWMVEVMSYGERPYWDMTNQDVINAIEDYRLPPMDPCPSALH 840
Db 781 AIQYRKFTSASDVMSYGIWMVEVMSYGERPYWDMTNQDVINAIEDYRLPPMDPCPSALH 840
QY 841 QLMDCWQKDRHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPLDRTIPDYTSFN 900
Db 841 QLMDCWQKDRHRPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPLDRTIPDYTSFN 900

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Fri Feb 1 11:16:32 2002

us-09-378-759-11.rapm

Db 841 QLMDCWQDRNHRPKFQIIVNTLDMIRNPNSLKAMAPLSSGINLPLLDRTIPDYTSN 900  
Qy 901 TVDEWLEAIKMGQYKESFANAGTSPFVVSQMMEDILRVGVTLAGHOKKILNSIQVMRA 960  
Db 901 TVDEWLEAIKMGQYKESFANAGTSPFVVSQMMEDILRVGVTLAGHOKKILNSIQVMRA 960  
Qy 961 QMNOIQSVEV 970  
Db 961 QMNOIQSVEV 970

RESULT 4  
US-08-235-407-2  
; Sequence 2, Application US/08235407  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; APPLICANT: Henkemeyer, Mark  
; TITLE OF INVENTION: NOVEL NEURAL KINASE AND RECEPTOR  
; TITLE OF INVENTION: TYROSINE KINASE  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bereskin & Parr  
; STREET: 40 King Street West, Box 401  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5H 3Y2  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/235,407  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kurdydyk, Linda M  
; REGISTRATION NUMBER: 34,971  
; REFERENCE/DOCKET NUMBER: 3153-82  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 364-7311  
; TELEFAX: (416) 361-1398  
; TELEX: 06-23115  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 994 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; ORIGINAL SOURCE:  
; ORGANISM: Mus musculus  
; DEVELOPMENTAL STAGE: Embryo  
; IMMEDIATE SOURCE:  
; LIBRARY: lambda gt10 cDNA library  
; CLONE: Combined pNKRACE A2 and K2 and cDNA clones  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: Distal end of chromosome 4  
; MAP POSITION: near the ahd-1 mutation  
US-08-235-407-2

Query Match 99.38; Score 5082; DB 6; Length 994;  
Best Local Similarity 99.28; Pred. No. 0;  
Matches 964; Conservative 4; Mismatches 2; Indels 1;  
Gaps 1;

Qy 1 LLAAYVEETLMDSTTATAELGWMVHPSPGWEVSGYDENNMNIRTYQVCNVFPESQNNWLR 60  
Db 23 LLAAYVEETLMDSTTATAELGWMVHPSPGWEVSGYDENNMNIRTYQVCNVFPESQNNWLR 82  
Qy 61 TKFIRRRGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSLATKTFPNWME 120

Db 83 TKFIRRRGAHRIHVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSLATKTFPNWME 142  
Qy 121 WKYVDTIAADSFQSDVLGGRVMKINTVRSFGPVSRSGFYLAQDYGGCMLIAVRVY 180  
Db 143 WKYVDTIAADSFQSDVLGGRVMKINTVRSFGPVSRNGFYLAQDYGGCMLIAVRVY 202  
Qy 181 RKCPLRIONGAIFQETLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGR 240  
Db 203 RKCPLRIONGAIFQETLSGABSTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPIGR 262  
Qy 241 MCKAGFEAVENGTVCRGCPSTGTFKANQGDGACTHCPINSRTTSEGATNCVCRNGYIRADL 300  
Db 263 MCKAGFEAVENGTVCRGCPSTGTFKANQGDGACTHCPINSRTTSEGATNCVCRNGYIRADL 322  
Qy 301 DPLDMPCCTTIPSAQAVISSVNETSLMLEWTTPRDSGGREDLVYNIICKSCGSGRGACTR 360  
Db 323 DPLDMPCCTTIPSAQAVISSVNETSLMLEWTTPRDSGGREDLVYNIICKSCGSGRGACTR 382  
Qy 361 CGDNVQYAPRQLGLTEPRYIYISDLLAHTQYTFEIQAVNGVTDQSPFQFASVNTTNOA 420  
Db 383 CGDNVQYAPRQLGLTEPRYIYISDLLAHTQYTFEIQAVNGVTDQSPFQFASVNTTNOA 442  
Qy 421 APSAVSIMHOVSRTVDSITLSWSQDPQPNQGVILDYELQYKEKELSEYNATAIKSPNTVT 480  
Db 443 APSAVSIMHOVSRTVDSITLSWSQDPQPNQGVILDYELQYKEKELSEYNATAIKSPNTVT 502  
Qy 481 --GLKAGAIYVQVVRARTVAGYSGKMYFQTMTEAEYQTSIQEKLPLIGSSAAGLVF 538  
Db 503 VQGLKAGAIYVQVVRARTVAGYSGKMYFQTMTEAEYQTSIQEKLPLIGSSAAGLVF 562  
Qy 539 LIAVVVTAIVCNRGRFERADSEYTDKLOHVTSGHITPGMKIYIDPFTYEDPNEAVREFAK 598  
Db 563 LIAVVVTAIVCNRGRFERADSEYTDKLOHVTSGHITPGMKIYIDPFTYEDPNEAVREFAK 622  
Qy 599 EIDTSCVKIEQVIGAGEFGEVCSGHLKLPKREIFAIVAKTLKSGYTEKQRDRFLSEASIM 658  
Db 623 EIDTSCVKIEQVIGAGEFGEVCSGHLKLPKREIFAIVAKTLKSGYTEKQRDRFLSEASIM 682  
Qy 659 QOFDPNVHLEGVVTKSTPVMIITEFMEGSLDSFLRQNDGQFTVQLVGLMRLGIAAGM 718  
Db 683 QOFDPNVHLEGVVTKSTPVMIITEFMEGSLDSFLRQNDGQFTVQLVGLMRLGIAAGM 742  
Qy 719 KYLADMNVVRDLAARNILVNSLVCKVSDPGLSRFLSDDTSDPTYSALGGKPIRWTA 778  
Db 743 KYLADMNVVRDLAARNILVNSLVCKVSDPGLSRFLSDDTSDPTYSALGGKPIRWTA 802  
Qy 779 PEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMNODVINAIEQDYRLPPMDCPSA 838  
Db 803 PEAIQYRKFTSASDVMSYGIWMVMSYGERPYWDMNODVINAIEQDYRLPPMDCPSA 862  
Qy 839 LHQLMDCWQDRNHRPKFQIIVNTLDMIRNPNSLKAMAPLSSGINLPLLDRTIPDYTS 898  
Db 863 LHQLMDCWQDRNHRPKFQIIVNTLDMIRNPNSLKAMAPLSSGINLPLLDRTIPDYTS 922  
Qy 899 FNTVDWLEAIKMGQYKESFANAGTSPFVVSQMMEDILRVGVTLAGHOKKILNSIQVM 958  
Db 923 FNTVDWLEAIKMGQYKESFANAGTSPFVVSQMMEDILRVGVTLAGHOKKILNSIQVM 982  
Qy 959 RAQMNOIQSVEV 970  
Db 983 RAQMNOIQSVEV 994

RESULT 5  
US-08-727-463-2  
; Sequence 2, Application US/08727463  
; GENERAL INFORMATION:  
; APPLICANT: Pawson, Anthony  
; APPLICANT: Henkemeyer, Mark  
; APPLICANT: Letwin, Kenneth  
; TITLE OF INVENTION: NEURAL RECEPTOR TYROSINE KINASE  
; NUMBER OF SEQUENCES: 2



CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MERCHANT & GOULD  
 STREET: 3100 Northwest Center, 90 South Seventh Street  
 CITY: Minneapolis  
 STATE: Minnesota  
 COUNTRY: U.S.A.  
 ZIP: 55403-4131  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/727,463  
 FILING DATE: 18-OCT-1996  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mueller, Douglas P.  
 REGISTRATION NUMBER: 30,300  
 REFERENCE/DOCKET NUMBER: M&G 7933.89-US-WO  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (612) 332-5300  
 TELEFAX: (612) 332-9081  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 994 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Mus musculus  
 DEVELOPMENTAL STAGE: Embryo  
 IMMEDIATE SOURCE:  
 LIBRARY: lambda gt10 cDNA library  
 CLONE: Combined pNUKACE A2 and K2 and cDNA clones  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: Distal end of chromosome 4  
 MAP POSITION: near the ahd-1 mutation  
 US-08-727-463-2

Query Match 99.3%; Score 5082; DB 11; Length 994;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;  
 QY 1 LLAVEETLMDSTTATAELGVMVHPFSGWEEVSGYDENMNTIRTYQVCNVFESSQNNWLR 60  
 DB 23 LLAVEETLMDSTTATAELGVMVHPFSGWEEVSGYDENMNTIRTYQVCNVFESSQNNWLR 82  
 QY 61 TKFTRRGARRHIVEMKFSVRDCSSIPSPVPGCKETFLNLYYEAADFATKTPNNWNP 120  
 DB 83 TKFTRRGARRHIVEMKFSVRDCSSIPSPVPGCKETFLNLYYEAADFATKTPNNWNP 142  
 QY 121 WKVVDTTAADESFQVLDGRVVKINTEVRSFGVSRSGFYLAQDYGGCMSLIARVVFY 180  
 DB 143 WKVVDTTAADESFQVLDGRVVKINTEVRSFGVSRSGFYLAQDYGGCMSLIARVVFY 202  
 QY 181 RKPRIITQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPVIGRC 240  
 DB 203 RKPRIITQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPVIGRC 262  
 QY 241 MCKAGFEAVENGTVRCRCPSTGTFKANGDEACTHCIPNSRTTSEGATNCVCRNGYRADL 300  
 DB 263 MCKAGFEAVENGTVRCRCPSTGTFKANGDEACTHCIPNSRTTSEGATNCVCRNGYRADL 322  
 QY 301 DPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR 360  
 DB 323 DPLDMPCTTIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCSGRGACTR 382  
 QY 361 CGNVQYAPRQLGLTPRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQFASVNTTNOA 420  
 DB 383 CGNVQYAPRQLGLTPRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQFASVNTTNOA 442

QY 421 APSAVSINHQSRTVDSITLWSQDOPNGVILDYELQYVEKELSEYNATAIKSPNTVT 480  
 DB 443 APSAVSINHQSRTVDSITLWSQDOPNGVILDYELQYVEKELSEYNATAIKSPNTVT 502  
 QY 481 --GLKAGAIYVQVRARTVAGYSGMYFQMTAEYQTSIOEKPLIIGSSAAGLVF 538  
 DB 503 VOGLKAGAIYVQVRARTVAGYSGMYFQMTAEYQTSIOEKPLIIGSSAAGLVF 562  
 QY 539 LIAVVVIAIYCNRRGFERADSEYTDKLOHTYSGHITPGMKIYIDPFTYEDPNBAVREFAK 598  
 DB 563 LIAVVVIAIYCNRRGFERADSEYTDKLOHTYSGHITPGMKIYIDPFTYEDPNBAVREFAK 622  
 QY 599 EIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDLSEASIM 658  
 DB 623 EIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKSGYTEKORRDLSEASIM 682  
 QY 659 GQFDHPNVHLEGVVTYKSTPVMITTEFMENGSLDSFLRQNDGQFTVIQLVGLRGIAAGM 718  
 DB 683 GQFDHPNVHLEGVVTYKSTPVMITTEFMENGSLDSFLRQNDGQFTVIQLVGLRGIAAGM 742  
 QY 719 KYLADMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTVTSALGKGFPIRWTA 778  
 DB 743 KYLADMYVHRDLAARNILVNSLVCKVSDFGLSRLEDDTSDPTVTSALGKGFPIRWTA 802  
 QY 779 PEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWMDTNQDVINAIEDYRLPPMDCPSA 838  
 DB 803 PEAIQYRKFTSASDVMSYGIYVMEVMSYGERPYWMDTNQDVINAIEDYRLPPMDCPSA 862  
 QY 839 LHQLMLDCHQKORNRHPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPLDRTIPDVT 898  
 DB 863 LHQLMLDCHQKORNRHPKFGQIVNTLDKMRNPNSLKAMAPLSSGINLPLDRTIPDVT 922  
 QY 899 FNTVDEWLEAIKMGQYKESFANAGFTSFVWSQMMEDILRVGVTLAGHOKKILNSIQVM 958  
 DB 923 FNTVDEWLEAIKMGQYKESFANAGFTSFVWSQMMEDILRVGVTLAGHOKKILNSIQVM 982  
 QY 959 RAQMNOIQSVEV 970  
 DB 983 RAQMNOIQSVEV 994

RESULT 6  
 US-08-727-463-2  
 ; Sequence 2, Application US/08727463A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PAWSON, ANTHONY  
 ; APPLICANT: HENKEMEYER, MARK  
 ; APPLICANT: LETWIN, KENNETH  
 ; APPLICANT: MOUNT SINAI HOSPITAL CORPORATION  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING SUBSTANCES AFFECTING RECEPTOR  
 ; TITLE OF INVENTION: TYROSINE KINASE ACTIVITY (AS AMENDED)  
 ; FILE REFERENCE: 7933.89USWO  
 ; CURRENT APPLICATION NUMBER: US/08/727,463A  
 ; CURRENT FILING DATE: 1997-03-11  
 ; EARLIER APPLICATION NUMBER: PCT/CA95/00254  
 ; EARLIER FILING DATE: 1995-04-28  
 ; EARLIER APPLICATION NUMBER: 08/235,407  
 ; EARLIER FILING DATE: 1994-04-29  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 994  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-08-727-463-2

Query Match 99.3%; Score 5082; DB 11; Length 994;  
 Best Local Similarity 99.2%; Pred. No. 0;  
 Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;  
 QY 1 LLAVEETLMDSTTATAELGVMVHPFSGWEEVSGYDENMNTIRTYQVCNVFESSQNNWLR 60



```

Db 323 DPLDMPCITIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 382
Qy 361 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQFASVNTTNOA 420
Db 383 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQFASVNTTNOA 442
Qy 421 APSAVSIMHQSRTVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSPTNTVT 480
Db 443 APSAVSIMHQSRTVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSPTNTVT 502
Qy 481 --GLKAGAIYVQVRAVYAGYSGKMYFQTMTEAETYSIOEKLPLITIGSSAAGLVF 538
Db 503 VQGLKAGAIYVQVRAVYAGYSGKMYFQTMTEAETYSIOEKLPLITIGSSAAGLVF 562
Qy 539 LIYVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTFCMKIYIDPFTYEDPNEAVREFAK 598
Db 563 LIYVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTFCMKIYIDPFTYEDPNEAVREFAK 622
Qy 599 EIDISCVKIEQVIGAGEGVCVSHLKLPGKREIFVAIKTLKSGYTEKQRDRFLSEASIM 658
Db 623 EIDISCVKIEQVIGAGEGVCVSHLKLPGKREIFVAIKTLKSGYTEKQRDRFLSEASIM 682
Qy 659 GQFDHPNVHLEGVYVTKSTPVMIIITEFMEGSLDSFLRQNDGQFTVIQLVGMRLGIAAGM 718
Db 683 GQFDHPNVHLEGVYVTKSTPVMIIITEFMEGSLDSFLRQNDGQFTVIQLVGMRLGIAAGM 742
Qy 719 KYLADMYVHRDLAARNILVNSLVCKVSDFGLSRFLEDDTSDPTTYSALGKFPPIRWTA 778
Db 743 KYLADMYVHRDLAARNILVNSLVCKVSDFGLSRFLEDDTSDPTTYSALGKFPPIRWTA 802
Qy 779 PEATQYRKFTSASDWISGVIMVEMVSGYGRPYWDMTNDQVINAEQDYRLPPMDCPSA 838
Db 803 PEATQYRKFTSASDWISGVIMVEMVSGYGRPYWDMTNDQVINAEQDYRLPPMDCPSA 862
Qy 839 LHQLMDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPLDRTIPDYS 898
Db 863 LHQLMDCWQKDRNHRPKFGQIVNTLDMIRNPNLSKAMAPLSSGINLPLDRTIPDYS 922
Qy 899 FNTVDEWLEAIKMGQYKESFANAGFTSFDFVVSQMMEDILRVGVTLAGHOKKILNSIQVM 958
Db 923 FNTVDEWLEAIKMGQYKESFANAGFTSFDFVVSQMMEDILRVGVTLAGHOKKILNSIQVM 982
Qy 959 RAQNMNQISQVEV 970
Db 983 RAQNMNQISQVEV 994

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RESULT 8

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US-08-730-700A-2
; Sequence 2, Application US/08730700A
; GENERAL INFORMATION:
; APPLICANT: Pawson, Anthony
; APPLICANT: Henkemeyer, Mark
; TITLE OF INVENTION: Method of Activating a Novel Ligand
; TITLE OF INVENTION: Regulatory Pathway
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Room 970
; STREET: 600 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1X5
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/730,700A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 60/005,518
; FILING DATE: 13-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurydyk, Linda M.
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 416-586-3235
; TELEFAX: 416-586-3110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 994 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-730-700A-2

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Query Match          99.3%; Score 5082; DB 11; Length 994;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

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Qy 1 LLAAVEETLMDSTTATAELGMVHPPSGWEEVSGYDENMNTIRTYQVCNVFESSQNNWLR 60
Db 23 LLAAVEETLMDSTTATAELGMVHPPSGWEEVSGYDENMNTIRTYQVCNVFESSQNNWLR 82
Qy 61 TKFIRRGAAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSDATKTFPNMNEP 120
Db 83 TKFIRRGAAHRHIVEMKFSVRDCSSIPSPGCKETFNLYYYEADFSDATKTFPNMNEP 142
Qy 121 WKVDTPIAADEFSQVDLGGRYMKINTEVRSFSPVSRSGFYLAFOYDGCNSLIAVRVFPY 180
Db 143 WKVDTPIAADEFSQVDLGGRYMKINTEVRSFSPVSRSGFYLAFOYDGCNSLIAVRVFPY 202
Qy 181 RKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEEDVDPIKLYCNGDGMWLPIGRC 240
Db 203 RKCPRIIQNGAIFQETLSGAESTSLVAARGSCIANAEEDVDPIKLYCNGDGMWLPIGRC 262
Qy 241 MCKAGFEAVENGTCVRCGCPSTGTFKANQDGEACTHCPINSRTTSEGATNCVCRNGYRADL 300
Db 263 MCKAGFEAVENGTCVRCGCPSTGTFKANQDGEACTHCPINSRTTSEGATNCVCRNGYRADL 322
Qy 301 DPLDMPCITIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 360
Db 323 DPLDMPCITIPSAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSCGSGRGACTR 382
Qy 361 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQFASVNTTNOA 420
Db 383 CGDNVQYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDQSPFSPQFASVNTTNOA 442
Qy 421 APSAVSIMHQSRTVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSPTNTVT 480
Db 443 APSAVSIMHQSRTVDSITLSWSQDPQNGVILDYELQYKEKELSEYNATAIKSPTNTVT 502
Qy 481 --GLKAGAIYVQVRAVYAGYSGKMYFQTMTEAETYSIOEKLPLITIGSSAAGLVF 538
Db 503 VQGLKAGAIYVQVRAVYAGYSGKMYFQTMTEAETYSIOEKLPLITIGSSAAGLVF 562
Qy 539 LIYVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTFCMKIYIDPFTYEDPNEAVREFAK 598
Db 563 LIYVVVIAIVCNRRGFERADSEYTDKLOHYTSGHMTFCMKIYIDPFTYEDPNEAVREFAK 622
Qy 599 EIDISCVKIEQVIGAGEGVCVSHLKLPGKREIFVAIKTLKSGYTEKQRDRFLSEASIM 658
Db 623 EIDISCVKIEQVIGAGEGVCVSHLKLPGKREIFVAIKTLKSGYTEKQRDRFLSEASIM 682
Qy 659 GQFDHPNVHLEGVYVTKSTPVMIIITEFMEGSLDSFLRQNDGQFTVIQLVGMRLGIAAGM 718
Db 683 GQFDHPNVHLEGVYVTKSTPVMIIITEFMEGSLDSFLRQNDGQFTVIQLVGMRLGIAAGM 742
Qy 719 KYLADMYVHRDLAARNILVNSLVCKVSDFGLSRFLEDDTSDPTTYSALGKFPPIRWTA 778

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Db	743	KYLAADMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTYSALGGKIPIRWTA	802
Qy	779	PEAIQYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVINAIEQDYELPPPMDCPSA	838
Db	803	PEAIQYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVINAIEQDYELPPPMDCPSA	862
Qy	839	LHQLMDCQKDRNHRKPGQIVNTLDMKIRNPNSLKAMAPLSSGINPLIDRTIPDYS	898
Db	863	LHQLMDCQKDRNHRKPGQIVNTLDMKIRNPNSLKAMAPLSSGINPLIDRTIPDYS	922
Qy	899	ENTVDEWLEAKMGQYKESFANAGFTSFDVVSOMMEDILRVGVTLAGHOKKILNSIQVM	958
Db	923	ENTVDEWLEAKMGQYKESFANAGFTSFDVVSOMMEDILRVGVTLAGHOKKILNSIQVM	982
Qy	959	RAQMNIQISVEV 970	
Db	983	RAQMNIQISVEV 994	
RESULT: 9			
US-09-621-595-2			
; Sequence 2, Application US/09621595			
; GENERAL INFORMATION:			
; APPLICANT: Pawson, Anthony			
; TITLE OF INVENTION: Method of Activating a Novel Ligand			
; Regulatory Pathway			
; NUMBER OF SEQUENCES: 21			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Room 970			
; STREET: 600 University Avenue			
; CITY: Toronto			
; STATE: Ontario			
; COUNTRY: Canada			
; ZIP: M5G 1X5			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/621,595			
; FILING DATE: 21-Jul-2000			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: 08/730,700			
; FILING DATE: <Unknown>			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Kurdydyk, Linda M.			
; REGISTRATION NUMBER: 34,971			
; REFERENCE/DOCKET NUMBER: 3153-196			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 416-586-3235			
; TELEFAX: 416-586-3110			
; INFORMATION FOR SEQ ID NO: 2:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 994 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:			
US-09-621-595-2			
Query Match 99.3%; Score 5082; DB 20; Length 994;			
Best Local Similarity 99.2%; Pred.No. 0;			
Matches 964; Conservative 4; Mismatches 2; Indels 2; Gaps 1;			
Qy	1	LLAAVEETLMDSTATAELGMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLR	60
Db	23	LLAAVEETLMDSTATAELGMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLR	82
RESULT 10			
US-09-194-755A-7			
; Sequence 7, Application US/09194755A			
; GENERAL INFORMATION:			
; APPLICANT: Matsui, Toshimitsu			
; TITLE OF INVENTION: Novel Human Receptor Type Tyrosine			
; KINASES: Kinases Like Protein			
; FILE REFERENCE: 07541.0001-00000			

; CURRENT APPLICATION NUMBER: US/09/194,755A  
 ; CURRENT FILING DATE: 1999-04-14  
 ; PRIOR APPLICATION NUMBER: PCT/JP97/01887  
 ; PRIOR FILING DATE: 1997-06-04  
 ; PRIOR APPLICATION NUMBER: JP 141849/1996  
 ; PRIOR FILING DATE: 1996-06-04  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 990  
 ; TYPE: PRT  
 ; ORGANISM: Rattus sp.  
 US-09-194-755A-7

Query Match 76.3%; Score 3901.5; DB 15; Length 990;  
 Best Local Similarity 73.5%; Pred. No. 4.2e-272;  
 Matches 717; Conservative 128; Mismatches 121; Indels 9; Gaps 3;

QY 2 LAAVEETLMDSTTATAEGLGMVHPSPGWEVSGYDENMTIRTYQVCNVFESSQNNWLR 61  
 DB 15 VAMEETLMDTTRTATAEGLGMVHPSPGWEVSGYDENMTIRTYQVCNVFESSQNNWLR 74  
 QY 62 KTRRRGAHRIHVEMKFSVRDSCSSIPSPGCKETENLYYEDFSDATKTFPNWENPW 121  
 DB 75 TFINRRGAHRIYTEMFTVRDSCSSLPNVPCKETENLYYEDFSDATKTFPNWENPW 134  
 QY 122 VKVDTTAADESEF-----QVDLGGVRMINTVRSFGPVSRSFGFLAFQDYGCGMSLTA 175  
 DB 135 LKVDTTAADESEFSSSSAAQVDFGGGLMKLVNTEVRSFGPLTRNGFLAFQDYGACMSL 194  
 QY 176 VRFYRKCPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEVLV 235  
 DB 195 VRFYRKCPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEVLV 254  
 QY 236 PIGRCMCKAGFAVENGVTCRCPSTFKANQGEACTHCPIINSTRTSEGATNCVCRNGY 295  
 DB 255 PIGRCMCKAGFAVENGVTCRCPSTFKANQGEACTHCPIINSTRTSEGATNCVCRNGY 313  
 QY 296 YRADLPLDMPCTTISAPQAVISSVNETSLMLETTPRDSGREDLVNITCKSGSGR 355  
 DB 314 YRADLPLDMPCTTISAPQAVISSVNETSLMLETTPRDSGREDLVNITCKSGSGR 373  
 QY 356 GACTRCGDNVQAPRGLGTEPRITYSIDLTAHTOYFEIQAVNGVTDQSPFQFASVNI 415  
 DB 374 RSCRCDDNVQAPRGLGTEPRITYSIDLTAHTOYFEIQAVNGVTDQSPFQFASVNI 433  
 QY 416 TTNQAAPSVMHQSATMRSTLSPQEPNGIILDEYIERYEKEHNEFNSSMARSO 475  
 DB 434 TTNQAAPSVMHQSATMRSTLSPQEPNGIILDEYIERYEKEHNEFNSSMARSO 493  
 QY 476 TWT--VTGLKAGAIYFQVARTVAGYGRYSKMYQTMTEAEYQTSIOEKPLITGSSA 533  
 DB 494 TWT--VTGLKAGAIYFQVARTVAGYGRYSKMYQTMTEAEYQTSIOEKPLITGSSA 553  
 QY 534 AGVFLIYAVVTAIVCNRRGERADESEYDKLOHYTSCHITPCMKIYIDPFYEDNEAV 593  
 DB 554 AGVFLIYAVVTAIVCNRRGERADESEYDKLOHYTSCHITPCMKIYIDPFYEDNEAV 613  
 QY 594 REFKEIDISCVKIEQVIGAGFEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDEFLS 653  
 DB 614 REFKEIDISCVKIEQVIGAGFEGVCSGHLKLPGRKEIFVAIKTLKSGYTEKORDEFLS 673  
 QY 654 EASIMQFDPHPNIVHLEGVYVTKSTPVMITFPMENGLSFLRQNDGQFTVQLVGLMRG 713  
 DB 674 EASIMQFDPHPNIVHLEGVYVTKSTPVMITFPMENGLSFLRQNDGQFTVQLVGLMRG 733  
 QY 714 IAAGMKYLADMYVHRDLAARILVNSLVCKVSDPGLSRFLEDDTSDTYTSALGGKFP 773  
 DB 734 IAAGMKYLADMYVHRDLAARILVNSLVCKVSDPGLSRFLEDDTSDTYTSALGGKFP 793  
 QY 774 IRWTAPEALQYRKFTSASDVWSYGIWMVMSYGERPYWDMTNOQVINAIEODYRLPPPM 833

DB 794 VRWTAPEALQYRKFTSASDVWSYGIWMVMSYGERPYWDMTNOQVINAIEODYRLPPPM 853  
 QY 834 DCPALHQLMLDCWOKDRHPRKFGOIVNTLDKMINPSLAKAMAPLSSGINPLDRTI 893  
 DB 854 DCPALHQLMLDCWOKDRHPRKFGOIVNTLDKMINPSLAKAMAPLSSGINPLDRTI 913  
 QY 894 PDYTSNTVDLEALIKMGQYKESFANAGTSPFDVYSOMMEDILRVGTLAGHOKKILN 953  
 DB 914 PDYTSNTVDLEALIKMGQYKESFANAGTSPFDVYSOMMEDILRVGTLAGHOKKILN 973  
 QY 954 SIQVMRAQMNQIQSV 968  
 DB 974 SIHSMRVQMNQSPSV 988

RESULT 11  
 US-07-861-390D-6  
 ; Sequence 6, Application US/07861390D  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PAWSON et al.  
 ; TITLE OF INVENTION: METHOD FOR EXPRESSING A  
 ; TITLE OF INVENTION: PHOSPHORYLATED PROTEIN  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Linda M. Kurdydyk, Bereskin & Parr  
 ; STREET: 40 King Street West, P. O. Box 401  
 ; CITY: Toronto, Ontario  
 ; STATE: N/A  
 ; COUNTRY: Canada  
 ; ZIP: M5H 3Y2  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: DOS Text File  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/861,390D  
 ; FILING DATE: 19920331  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: J.G. Mullins  
 ; REGISTRATION NUMBER: 33073  
 ; REFERENCE/DOCKET NUMBER: 027-021  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703) 684-1111  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1009 amino acids  
 ; TYPE: AMINO ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-07-861-390D-6

Query Match 73.0%; Score 3735; DB 3; Length 1009;  
 Best Local Similarity 71.3%; Pred. No. 4.5e-260;  
 Matches 708; Conservative 129; Mismatches 130; Indels 26; Gaps 13;

QY 2 LAAVEETLMDSTTATAEGLGMVHP--PSGWEVSGYDENMTIRTYQVCNV--PESSQNNWL 59  
 DB 15 VAMEETLMDTTRTATAEGLGMVHP--PSGWEVSGYDENMTIRTYQVCNV--PESSQNNWL 74  
 QY 60 RTKFIIRRRG-AHRIHVEMKFSVRDSCSSIPSPV--GSKETFNLYYEDFSDATKTFPNW 116  
 DB 75 LTFINRRGAHRIYTEMFTVRDSCSSLPNVPCKETENLYYEDFSDATKTFPNW 134  
 QY 117 MENPVKVTDTAADESEFSDVLDGGRVWKINTVRSFGPVSRSFGFLAFQDYGCGMSL 176  
 DB 135 SEAPYLKVDIIAADESEFSDVLDGGRVWKINTVRSFGPVSRSFGFLAFQDYGCGMSL 194  
 QY 177 RYFVKCPRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEVL 233

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Db 195 RVFFKKCPISVQNFVAFPEIMTGAESTSLVIARTGTCIPNAEVDVPPXXXIKLXNGDGEW 254
QY 234 LVPTGRCKWAGAEVNGVTCGCPSTGKANKOGDEACTHCPINSTRTTSEGTATNCVCRN 293
Db 255 WPIGRCTCKAGYEPENXVACKACAGTAKASOEGCSHCPSNSRSPSEAPICHTCRT 314
QY 294 GYRADLDPLDMPCTTPSPAQOAVISSV-NETSLMLEWTPPRDSGGREDIVYNIICKSCG 352
Db 315 GYRADDPPEVACTSPVSPGRNVISVXNETSILLEHHPHRETGGRDDTYNIICKKX 374
QY 353 SGRG---ACTRCGNVOYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPSPQ 409
Db 375 XRDARSRCSDCNDFEVPRQLGLTECRVSISSLWHTPTFTDIAINGVSSKSPFPQ 434
QY 410 -FASVNTTNOAPSAYSIMHO-VSRVDSITLSWSQDOPNGVILDYQYKEKLESEY 467
Db 435 HVXSVNTTNOAPSTVPIHQXVSATMRSTILSWPOEPNGIILDIYEIYKEKNEF 494
QY 468 NATAIKSPINT--VTGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAEAYQTSIQEKL 525
Db 495 NSSMARSQTNWARTIDGLRPGVYVQVARTVAGYGRYSGKMYFQMTIDDYKSELREL 554
QY 526 PLITGSSAAGLVFLIAVVIATVAVNRRGFERADSEYTDK-----LQHTSCHIITPMKIYI 581
Db 555 PLIAGSAAAGVVFVSVLAISIVCSRKAYSKEAVYSDKXXXLQHYSTGRGSPGKIYI 614
QY 582 DPFTYEDPNEAVREFAKEIDISCV-----KTEQVIGAGEFGEVCSGHLKLP-KREIFVA 635
Db 615 DPFIYEDPNEAVREFAKEIDVSFYVXXXKLEEVIGAGEFGEVYKGRKLPKGRKELIYA 674
QY 636 IKTLKSGYTEKQRDFTSEASIMQFQDHPNVIHLEGVVTKTSTPTVMIETEMENGLSDFL 695
Db 675 IKILKAGYSEKQRDFTSEASIMQFQDHPNIIRLEGVVTKSRPVMIIETEMENGALDSFL 734
QY 696 RQNDQFTVITOLVGLMGRGIAAGMYKADNMVVRHDLAARNILVNSLVCKVSDFLGREL 755
Db 735 RONDEQFTVITOLVGLMGRGIAAGMYKLEMMNVVRHDLAARNILVNSLVCKVSDFLGREL 794
QY 756 EDDTSDPTYSALGKFPRTWTAPEATQYRKFTSASDVMSYGIWVWVMSYGERPYWDMT 815
Db 795 QDDTSDPTYSALGKFPRTWTAPEATQYRKFTSASDVMSYGIWVWVMSYGERPYWDMS 854
QY 816 NQDVINAIEQDYLPPMDPCPSALHQLMDCQKDRNHRPKFGQIVNTLDMIRNPNSLK 875
Db 855 NQDVINAIEQDYLPPMDPCPSALHQLMDCQKDRNHRPKFGQIVNTLDMIRNPNSLK 914
QY 876 AMAPLSSGILNPLDRTIPDYTSFNTVDWLEATKMGQYKESFANAGFTSPDVVSQMMME 935
Db 915 TVATITAVPSQPLLDRTSIPDFTFTVDDWLSAIAKMWQYRDSFLTAGFTSLQLVTQMISE 974
QY 936 DILRVGVTLAGHQRKILNSIQVMRAQMNQISQV 968
Db 975 DILRIGVTLAGHQRKILNSIHSIMRVQMNQSPSV 1007

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RESULT 12

US-08-449-645-20

Sequence 20, Application US/08449645

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

APPLICANT: Welcher, Andrew A.

APPLICANT: Jing, Shuguan

TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,645
; FILING DATE: May 24, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287-A
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-449-645-20

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Query Match 71.0% Score 3632.5; DB 8; Length 998;

Best Local Similarity 70.5% Pred. No. 1-le-252;

Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

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QY 4 AVEETLMDSTTATAELGWMVHPSPGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKF 63
Db 37 ALEETLMDTKVWTSELAWTSHPSGWEVSGYDEAMPNIRTYQVCNVFESSQNNWLRTGF 96
QY 64 IRRGAGRIHVEMFSDYDCSSIPSPCKSETNLXYEADFSATKTFENWENPMVK 123
Db 97 IWRDVRVVYVELFTVRDCNSIPNPGCKSETNLFYEADSVASASSFWENPMVK 156
QY 124 VDTAADESFSQVDLGGVRMKINTEVRSFGVSRSGFLAFQDYGGCMSLIAVRVYRKC 183
Db 157 VDTAPDESFLDAG---RVNFKVRSFGPLSKAGFLAFQDQGACNSLISVRAFYKCC 212
QY 184 PRIOTNGAIFQETLSGAEKSTSLVAARGSCIANAEVDVPIKLYCNGDGEWLVPGRCKMCK 243
Db 213 ASATTAGFALFETLTGABPTSLVIAPTGTCIPNAVEVSPLKLYCNGDGEWMPVAGACTCA 272
QY 244 AGFEAVENGTVCRGCPGCTFKANOGDEACTHCPINSTRTTSEGTATNCVCRNVLRLDPL 303
Db 273 TGHEPAKESOCRCPPGSGYKAKOGEGCLPCPNSTRTTSPAASICTCHNNFYRADSDSA 332
QY 304 DMPCTTIPSPAQAVISSVNETSLMLEWTPPRDSGGREDLVYNIICKSC--GSGRGACTRC 361
Db 333 DSACTTVPSPRGVSNVNETSLILENSEPRDLGVRDLDLYNVICKKCHGAGGASACSRK 392
QY 362 GDNVOYAPRQLGLTEPRIYISDLAHTQYTFEIQAVNGVTDOSPSPQFASVNTTNOAA 421
Db 393 DDNVEFVPRQLGLSEPRVHTSHLLAHTRYTTEVOAVNGVSGKSPPLPPRYAAVNTTNOAA 452
QY 422 PSAYSIMHOVSRTVDSITLSWSQDOPNGVILDYQYKEKLESEYNATAIKSPNTV-- 479
Db 453 PSEVPTLRLHSSGSSSLTWAPERPNGVILDYEMKIFER--SEGIATVTSQNNVOL 510
QY 480 TGLKAGAIYVQVARTVAGYGRYSGKMYFQMTAE-AYQTSIQEKLPLIIGSSAAGLVF 538
Db 511 DGLRPDARYVQVARTVAGYGRYSGKMYFQMTAEFETTSERGSAQQLQEQPLVIGSATAGLVF 570
QY 539 LIAVVVIAVNCNRRGFERADSEYTDKLOHYTSGHITPMKMYIDPFTYEDNEAVREFAK 598
Db 571 VVAVVIAVCLRKORHGSDEYTEKLOQY----IAPGMKVYIDPFTYEDNEAVREFAK 626
QY 599 BIDSCYKIEQVIGAGEFGEVCSGHLKLPKGRKELFVALTKLSGYTEKORDFLSEASIM 658
Db 627 BIDSCYKIEEIVIGAGEFGEVGRGLKOPGRREVFALTKLVGYTERQRDFLSEASIM 686
QY 659 QQFDPNVIHLEGVVTKTSTPTVMIETEMENGLSDFLRQNDQFTVITOLVGLMGRGIAAGM 718
Db 687 QQFDPNIIRLEGVVTKSRPVMIIETEMENGALDSFLRNDQFTVITOLVGLMGRGIAAGM 746

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QY 719 KYLADMYVHRDLAARNILVNSNLVCKVSDGLSRFLEDDTSDPTTYSALGKPIRWTA 778  
DB KYLSEMYVHRDLAARNILVNSNLVCKVSDGLSRFLEDDTSDPTTYSALGKPIRWTA 806  
QY 779 PEAIQYRKFTSASDWSYGIWMEVMSYGERPYWDMNQDVINAIEQDYRLPPMDCPSA 838  
DB PEAIQYRKFTSASDWSYGIWMEVMSYGERPYWDMNQDVINAIEQDYRLPPMDCPSA 866  
QY 839 LHQLMDCWDRNLRPKFSQIVNTLDKLRNPNLSKAMAPLSGGINLPDLRTIPDYS 898  
DB LHQLMDCWDRNLRPKFSQIVNTLDKLRNPNLSKAMAPLSGGINLPDLRTIPDYS 926  
QY 899 FNTVDEWLEAKMGQYKESFANAGFTSFVVSQMMEDILRVGYTLAGHQKILNSIQVM 958  
DB FNTVDEWLEAKMGQYKESFANAGFTSFVVSQMMEDILRVGYTLAGHQKILNSIQVM 986  
QY 959 RAQMNIQSVQV 970  
DB RAQMNIQSVQV 998

## RESULT 13

US-08-702-367-20  
; Sequence 20, Application US/08702367  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/702,367  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/229,509  
; FILING DATE: 15-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-287  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 998 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-702-367-20

Query Match 71.0%; Score 3632.5; DB 11; Length 998;  
Best Local Similarity 70.5%; Pred. No. 1.1e-252;  
Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

QY 4 AVEETLMDSTTAEALGMVHPSPGWEESGVDENMTITVQVNCVFPSSQNNWLRKTF 63  
DB ALETLMKTKWVTELAWSHPGWEESGVDENMTITVQVNCVFPSSQNNWLRKTF 96  
QY 64 IRRRGARRHVKFSDVCSIPSPGCKETFNLYYEADFSATKTFPNMKNPWVK 123  
DB IRRRGARRHVKFSDVCSIPSPGCKETFNLYYEADFSATKTFPNMKNPWVK 156

QY 124 VDTIAADESESOVDLGRVMKINTEVSRGVPVSRSGPYLAFQDYGCGCMSLIAVRFYRKC 183  
DB VDTIAPDESFSRLDAG----RVNTKVSFGPLSKAGPYLAFQDQAGCMCLISVRAFYRKC 212  
QY 184 PRITQNGAIFQETLSGAESTSLVAARGSCIANABEVDPVPIKLYCNGDGEWLVPICGMCK 243  
DB ASTTAGFALPETLTGAETPSLVAPCTCIPNAVEVSVPKLKLYCNGDGEWMPVAGTCA 272  
QY 244 AGPRAVNGTVRCGCPSTGTPKANOGDEACHTCPINSTRTTSEGTNCVCRNGYRADIPL 303  
DB TGHEPAAKESQCRPPGSGYKAKQEGECLPCPPNSRTTSPAAISICTCHNNFRADSDA 332  
QY 304 DMCPTTIPSAOAVISSVNETSLMLETTPRDSGREDLVNIIKSC--GSGRGACTRC 361  
DB DSACTTVSPRGVSNVNETSLLEWSEPRDLGVRODLLNVJCKKCHGAGGASASRC 392  
QY 362 GDNVQYAPRQLGTEPRIYISDLIAHTQYTFEIQAVNGVTDQSPFSPQFASVNTTNOAA 421  
DB DDNEFVPRQLGLSEPRVHTSHLLAHTRYTFEQAVNGVSGKSPPLPPRYAANVTNOAA 452  
QY 422 PSAVSIHQVSRVDSITLSNSQPDQNGVILDYELQYKEKELSEYNATAIKSPTNTV-- 479  
DB PSEVPTLRLHSSGSLTSLWAPPERPNGVILQYEMKYFEK--SEGIASVTISQMSVOL 510  
QY 480 TGLKAGAIYVFOVARTVAGYSGYSGKMYFQMTWE-AEYQTSIQEKLPLIGSSAAGLVF 538  
DB DGLRDPARYVQVARTVAGYQYSRPAEFETTSERGSGAQQLQEQPLIVGSATAGLVF 570  
QY 539 LIAVVIATVNCRRGERADSEYTDKLOHYTSGHIPTGMKIYIDPFTYEDPNEAVREFAK 598  
DB VVAVVVIATVNCRRGERADSEYTDKLOHYTSGHIPTGMKIYIDPFTYEDPNEAVREFAK 626  
QY 599 EIDISCVKIEQVIGAGEFGEVCSGHLKLPKRIEFAIKTLKSGYTEKQRDRFLSEASIM 658  
DB EIDVSCVKIEEIVIGAGEFGEVCSGHLKLPKRIEFAIKTLKSGYTEKQRDRFLSEASIM 686  
QY 659 GQFDHPNVHLEGVVTKSTPVMILTEFMENGSLDSFLRQNDGQFTVQLVGLMGTAAAG 718  
DB GQFDHPNVHLEGVVTKSTPVMILTEFMENGSLDSFLRQNDGQFTVQLVGLMGTAAAG 746  
QY 719 KYLADMYVHRDLAARNILVNSNLVCKVSDGLSRFLEDDTSDPTTYSALGKPIRWTA 778  
DB KYLSEMYVHRDLAARNILVNSNLVCKVSDGLSRFLEDDTSDPTTYSALGKPIRWTA 806  
QY 779 PEAIQYRKFTSASDWSYGIWMEVMSYGERPYWDMNQDVINAIEQDYRLPPMDCPSA 838  
DB PEAIQYRKFTSASDWSYGIWMEVMSYGERPYWDMNQDVINAIEQDYRLPPMDCPSA 866  
QY 839 LHQLMDCWDRNLRPKFSQIVNTLDKLRNPNLSKAMAPLSGGINLPDLRTIPDYS 898  
DB LHQLMDCWDRNLRPKFSQIVNTLDKLRNPNLSKAMAPLSGGINLPDLRTIPDYS 926  
QY 899 FNTVDEWLEAKMGQYKESFANAGFTSFVVSQMMEDILRVGYTLAGHQKILNSIQVM 958  
DB FNTVDEWLEAKMGQYKESFANAGFTSFVVSQMMEDILRVGYTLAGHQKILNSIQVM 986  
QY 959 RAQMNIQSVQV 970  
DB RAQMNIQSVQV 998

## RESULT 14

US-09-378-759-20  
; Sequence 20, Application US/09378759  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Gary M.  
; TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine  
; TITLE OF INVENTION: Kinases  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Patent Operations/RBW  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks

STATE: California  
 COUNTRY: USA  
 ZIP: 91320  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/378,759  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/702,367  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE/DOCKET NUMBER: A-287  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 998 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-378-759-20

Query Match 71.0%; Score 3632.5; DB 17; Length 998;  
 Best Local Similarity 70.5%; Pred. No. 1.1e-252;  
 Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

QY 4 AVEETLMDSSTTAAELGMMVHPSPGSEWEEVSGYDENMNTTIRTYQVNCVFPSSONNMLRTKF 63  
 DB 37 ALEETLMDTKWTVSELAWTSHPESEWEEVSGYDEAMNPRTTYQVNCVFPSSONNMLRTGF 96

QY 64 IRRGAHRHIVEMKFSVRDCSSIPSPGSKCTFNLYYEADFDTSATKTFPNMNMENPWYK 123  
 DB 97 IWRDQVRVYVELKFTVRDCNSIPNIPGSKCTFNLYYEADSDVASASPPFWMENPYVK 156

QY 124 VDTIADESFSQVDLGGGRVYKINTEVRSFGPVSRGFFLAFOYGGCMLIAVRFPYKRC 183  
 DB 157 VDTIAPDESFSRLDAG----RVNTKVRSPGLSKAGFYLAFOYGGCMLISVRAFYKRC 212

QY 184 PRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPYIGRCMCK 243  
 DB 213 ASTTAGFALFPELTGAETPSLVIAPICTIPNAVEVSPVPLKLYCNGDGEWLPVVGACTCA 272

QY 244 AGFEAVENGTVCRCGSPGTFKANOQDEACTHCPINRSRTTSEGATNCVCRNGYYRADLDPL 303  
 DB 273 TGHEPAAKESQCRPCPPGSKYKAKQGBGCLPCPPNSRTTSPAASICTCHNFFYRADSDSA 332

QY 304 DMPCTTIPSAQNAVSSVNETSLMELWTPRSGGREDLYVNIICKSC--GSGRGACTRC 361  
 DB 333 DSACTVTPSPRGVSNVNETSLILEWSEPRDLGVDRDLYLVNICKKCHAGGASACSR 392

QY 362 GDNVYAPRLGLTEPRIVISDLAHTQTFEIQAVNGVTDQSPFQSFASVNIITNQAA 421  
 DB 393 DNVFVFPQLGLSEPRVHTSHLLAHTRTFFVQAVNGVSGKSPPLPRYAANVNIITNQAA 452

QY 422 PSASVIMHVSRTVDITLSWQSDQPNVILDEYLOYYEKELESEYNATAIKSPNTV-- 479  
 DB 453 PSEVPTLRLHSSSGSLTSLWAPPRPNVGVLDYEMKYEK--SEGIASTVTSQMSVOL 510

QY 480 TGLKAGAIYVQVRAKTAVAGYGRYSKMYFOIWTAEYQTSQKLEPLTIGSSAGLVF 538  
 DB 511 DGLRDPARYVQVRAKTAVAGYGRYSKMYFOIWTAEYQTSQKLEPLTIGSSAGLVF 570

QY 539 LIAYVVAIVCNRRGPERASEYTDKLOHYTSGHIPGKMYIDPTTYEDPDNEAVREFAK 598  
 DB 571 VVAVVVAIVCLRKORHSDSEYTEKLOQY----IAPGMKVIIDPTTYEDPDNEAVREFAK 626

QY 599 EIDISCVKIEQVIGAGEFGEVCGHKLKPGKREIFVAIKTLKSGYTEKQRRDFLSEASIM 658

DB 627 EIDVSCVKIEVIGAGEFGEVCGHKLKPGKREIFVAIKTLKSGYTERQRRDFLSEASIM 686

QY 659 GQFDHPNVIHLEGVVTKSTPMIITEFMEGSLDSELRNDQGFVQLVGLMGLRGIAAGM 718

DB 687 GQFDHPNIIIRLEGVVTKSRPVIITEFMEGSLDSELRNDQGFVQLVGLMGLRGIAAGM 746

QY 719 KYLADMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTTYSALGKGFPIRWTA 778

DB 747 KYLSEMYVHRDLAARNILVNSLVCKVDFGLSRFLEDDTSDPTTYSALGKGFPIRWTA 806

QY 779 PEATYRKFTSASDVMSYGVIMVWVMSYGERPYWDMNQDVINAIEQDYRLPPLPMDCPSA 838

DB 807 PEATYRKFTSASDVMSYGVIMVWVMSYGERPYWDMNQDVINAIEQDYRLPPLPMDCPSA 866

QY 839 LHOMLDCWQKDRNHRPKFGOIVNTLDKMIKRNPSLKAMAPLSSGINKLPLDRIPTDPTS 898

DB 867 LHOMLDCWVRDNRNLRPKFSQIVNTLDKLIIRNAASLKVIASQAQSGMSQPLLDRIPTDPT 926

QY 899 FNTVDLEWLEAIKMGQYKESFANAGFTSPDVVVSQMMEDILRVGVTLAGHQKILNSIQVM 958

DB 927 FTTVGDWLDAIKMGYKESFVSAGFASFDLVQAQTAEDLLRIGVTLAGHQKILNSIQDM 986

QY 959 RAQMNQIQSVFV 970

DB 987 RLOMNQTLPPVQV 998

RESULT 15  
 PCT-US01-03800A-2273  
 ; Sequence 2273, Application PC/TUS0103800A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; APPLICANT: Tang, Y, Tom et al  
 ; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides  
 ; FILE REFERENCE: 21272-030  
 ; CURRENT APPLICATION NUMBER: PCT/US01/03800A  
 ; CURRENT FILING DATE: 2001-02-05  
 ; PRIOR APPLICATION NUMBER: 09/560,875  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 09/496,914  
 ; PRIOR FILING DATE: 2000-02-03  
 ; NUMBER OF SEQ ID NOS: 2700  
 ; SOFTWARE: Custom  
 ; SEQ ID NO 2273  
 ; LENGTH: 1007  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 PCT-US01-03800A-2273

Query Match 71.0%; Score 3632.5; DB 1; Length 1007;  
 Best Local Similarity 70.5%; Pred. No. 1.1e-252;  
 Matches 685; Conservative 114; Mismatches 158; Indels 15; Gaps 6;

QY 4 AVEETLMDSSTTAAELGMMVHPSPGSEWEEVSGYDENMNTTIRTYQVNCVFPSSONNMLRTKF 63  
 DB 46 ALEETLMDTKWTVSELAWTSHPESEWEEVSGYDEAMNPRTTYQVNCVFPSSONNMLRTGF 105

QY 64 IRRGAHRHIVEMKFSVRDCSSIPSPGSKCTFNLYYEADFDTSATKTFPNMNMENPWYK 123  
 DB 106 IWRDQVRVYVELKFTVRDCNSIPNIPGSKCTFNLYYEADSDVASASPPFWMENPYVK 165

QY 124 VDTIADESFSQVDLGGGRVYKINTEVRSFGPVSRGFFLAFOYGGCMLIAVRFPYKRC 183  
 DB 166 VDTIAPDESFSRLDAG----RVNTKVRSPGLSKAGFYLAFOYGGCMLISVRAFYKRC 221

QY 184 PRIQNGAIFQETLSGAESTSLVAARGSCIANAEVDVPIKLYCNGDGEWLPYIGRCMCK 243  
 DB 222 ASTTAGFALFPELTGAETPSLVIAPICTIPNAVEVSPVPLKLYCNGDGEWLPVVGACTCA 281

QY 244 AGFEAVENGTVCRCGSPGTFKANOQDEACTHCPINRSRTTSEGATNCVCRNGYYRADLDPL 303



Db 282 TGHEPAAKESQCRPCPGSYKQKQEGECLPCPPNSRTTSPAASICTCHNNFYRADSDSA 341  
QY 304 DMCCTTIPSAPOAVISSVNETSLMELWTPRDSGREDLVNIIICKSC--GSGRGACTRC 361  
Db 342 DSACTTVSPRGVINSVNETSLLEWSEPRDLGVDRDLDLYNVICKKCHGAGGASACSRC 401  
QY 362 GDNVQYAPROLGLTEPRYIYISDLIAHTQYTFEIQAVNGVTDQSPFSQFASVNTITNOAA 421  
Db 402 DDNVFVPRQLGLSEPRVHTSHLLAHTRYTFEQAVNGVSGKSPPLPPRYAAVNITITNOAA 461  
QY 422 PSASVIMHQSRTVDSITLSKSGQDPQNGVILDYELQYKEKELSEYNATAIKSPTNTV-- 479  
Db 462 PSEVPTLRLHSSGSSLTLSWAPPERPNGVILDYEMKYFEK--SEGIASTVTSQMNVSQVL 519  
QY 480 TGLKAGAIYVFOVARTVAGYGRYSGKMYQTWTE-AEYQTSIQEKLPLIIGSSAAGLVF 538  
Db 520 DGLRPDARYVQVARTVAGYQTSRAPEFETTSERGSGAQQLQOEQLPLIVGSATAGLVF 579  
QY 539 LIAVVVIAIYCNRRGERADSEYTDKLQHYTSGHITPGMKIYIDPFTYEDPNEAVREFAK 598  
Db 580 WVAVVVIAIYCLRKQRHGSDEYTEKLQY----IAPGMKYIDPFTYEDPNEAVREFAK 635  
QY 599 EIDISCVKIEQVTCAGGEFVCGSHLKLPGKREIFVAIKTLKSGYTEKQRDFLSEASIM 658  
Db 636 EIDVSCVKIEEVIGAGEFVCGRLKQPGRRREVFAIKTLKVGYTEQRDRDFLSEASIM 695  
QY 659 GQFDHPNVIHLEGVVTKSTPVMILTEFMENGLDSELRQNDGQFTVQLVGMRLGTAAGM 718  
Db 696 GQFDHPNIIILEGVVTKSRPVMILTEFMENCALDSELRQNDGQFTVQLVGMRLGTAAGM 755  
QY 719 KYLADNMVYHRDLAARNILVNSNLCKVSDFGLSRFELEDDTSDPTVTSALGKGFPIRWTA 778  
Db 756 KYLSENNVYHRDLAARNILVNSNLCKVSDFGLSRFELEDDTSDPTVTSALGKGFPIRWTA 815  
QY 779 PEAIQYRKFTSASDVWSYGIWMEVMSYGERPYWDMTNQDVINAIEDQYRLPPPMDCPSA 838  
Db 816 PEAIYRKFTSASDVWSYGIWMEVMSYGERPYWDMNSQDVINAVEQDYRLPPPMDCPTA 875  
QY 839 LHQLMLDCWQKDRNHRPKFGQIYVNTLDKMRPNNSLKAMAPLSSGINLPLLDRTIPDYTS 898  
Db 876 LHQLMLDCWVRDNRNLRPKFSQIYVNTLDKLIRNAASLKVIASAGSGMSQPLDRTVPDYTT 935  
QY 899 FNTVDWLEAIKMGQYKESFANAGFTSFVDSQMMMEDILRVGVTLAGHQKILNSIQVM 958  
Db 936 FTTVGDWLDIAIKMGYKESFVSAGFASFDLVAQWTAEDLLRIGVTLAGHQKILNSIQDM 995  
QY 959 RAQMNOIQSVEV 970  
Db 996 RLQMNQTLPVQV 1007

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Job time: 402 sec

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